

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2004, 08:49:47 ; Search time 37.7711 Seconds
(without alignments)
793.576 Million cell updates/sec

Title: US-09-996-617-2_COPY_1335_1429
Perfect score: 490
Sequence: 1 LHFVDYQRLIARTSVSEV.....HLIMELWKGSKGGLPLSS 95

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seg length: 0
Maximum DB seg length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL.25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rviro.*
16: sp_bacteriap.*
17: sp_archaeap.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	238	48.6	195	6 Q8HXK9	Q8HXK9 bos taurus
2	210	42.9	193	11 Q8CHK8	Q8CHK8 rattus norv
3	84.5	17.2	1175	16 Q8XNW6	Q8XNW6 clostridium
4	82.5	16.8	614	16 Q8ENW9	Q8ENW9 oceanobacil
5	79.5	16.2	260	2 Q8GBV1	Q8GBV1 pseudomonas
6	79.5	16.2	260	2 Q8G977	Q8G977 pseudomonas
7	79.5	16.2	338	2 Q9ZSV9	Q9ZSV9 pseudomonas
8	79.5	16.2	404	2 Q52212	Q52212 pseudomonas
9	79.5	16.2	425	2 Q9X7J2	Q9X7J2 pseudomonas
10	78	15.9	193	17 Q8ZSQ2	Q8ZSQ2 pyrobaculum
11	78	15.9	254	5 Q966F3	Q966F3 caenorhabdi
12	77.5	15.8	376	11 Q8K4E9	Q8K4E9 mus musculu
13	77.5	15.8	376	11 Q921F0	Q921F0 mus musculu
14	76	15.5	295	5 Q95018	Q95018 caenorhabdi
15	75	15.3	482	16 Q8YKJ7	Q8YKJ7 anabaena sp
16	74.5	15.2	734	2 Q84FL9	Q84FL9 pantoea agg

17	73.5	15.0	584	16 Q9PLZ8	Q9PLZ8 campylobact
18	73	14.9	376	11 Q8K4E7	Q8K4E7 mus musculu
19	72.5	14.8	630	11 Q8C2K1	Q8C2K1 mus musculu
20	72	14.7	175	16 Q8EPP9	Q8EPP9 oceanobacil
21	72	14.7	376	11 Q8K4E8	Q8K4E8 mus musculu
22	72	14.7	376	11 Q8K4E6	Q8K4E6 mus musculu
23	71.5	14.6	267	5 Q8BNF3	Q8BNF3 caenorhabdi
24	71.5	14.6	630	11 Q8OXA9	Q8OXA9 mus musculu
25	71	14.5	197	17 Q59062	Q59062 pyrococcus
26	70	14.3	251	11 Q8VI98	Q8VI98 mus musculu
27	70	14.3	252	11 Q8JZN4	Q8JZN4 mus musculu
28	70	14.3	315	11 Q9CRP3	Q9CRP3 mus musculu
29	70	14.3	376	11 Q8JZNO	Q8JZNO mus musculu
30	70	14.3	592	16 Q81TV0	Q81TV0 bacillus an
31	70	14.3	691	16 Q9EP55	Q9EP55 mycoplasma
32	70	14.3	870	5 Q9GQ59	Q9GQ59 strongyloce
33	69.5	14.2	96	10 Q8LSL7	Q8LSL7 vitis vinif
34	69.5	14.2	453	13 Q801R9	Q801R9 xenopus lae
35	69.5	14.2	603	13 Q92021	Q92021 xenopus lae
36	69	14.1	379	11 Q70522	Q70522 rattus norv
37	69	14.1	406	5 Q17460	Q17460 schistosoma
38	69	14.1	788	12 Q91NQ3	Q91NQ3 prune dwarf
39	69	14.1	870	2 Q84HV6	Q84HV6 anaplasma m
40	69	14.1	871	16 Q9X1R4	Q9X1R4 thermotoga
41	68.5	14.0	610	13 Q91431	Q91431 xenopus lae
42	68.5	14.0	771	13 Q918K4	Q918K4 rana catesb
43	68	13.9	265	16 Q81GN8	Q81GN8 bacillus ce
44	68	13.9	368	10 Q41236	Q41236 solanum tub
45	68	13.9	1816	12 Q91WB1	Q91WB1 soil-borne

ALIGNMENTS

RESULT 1

Q8HXK9
ID Q8HXK9 PRELIMINARY; PRT; 195 AA.
AC Q8HXK9
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, last sequence update)
DE 01-JUN-2003 (TRENBLrel. 24, last annotation update)
DE Apoptosis-associated speck-like protein containing a CARD.
GN BASC.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Masumoto J., Zhou W., Chen F.F., Su F., Kuwada J.Y., Hidaka E.,
RA Katsuyama T., Sagara J., Taniguchi S., Ngo-Hazelett P.,
RA Postlethwait J.H., Nunez G., Inohara N.,
RT "Casp-1: A Zebrafish caspase activated by ASC oligomerization required
for pharyngeal Arch development.";
RL J. Biol. Chem. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20036508; PubMed=10567338;
RA Masumoto J., Taniguchi S., Ayukawa K., Sarvotham H., Kishino T.,
RA Niihara N., Hidaka E., Katsuyama T., Higuchi I., Sagara J.; of human
RT "ASC, a novel 22-kDa protein, aggregates during apoptosis of human
promyelocytic leukemia HL-60 cells.";
RL J. Biol. Chem. 274:33835-33838(1999).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20580347; PubMed=11139337;
RA Masumoto J., Taniguchi S., Nakayama K., Ayukawa K., Sagara J.;
RT "Murine ortholog of ASC, a CARD-containing protein, self-associates,
and exhibits restricted distribution in developing mouse embryos.";
RL Exp. Cell Res. 262:128-133(2001).
DR EMBL; AB050006; BAC43753.1;
GO; GO:0005622; Cintracellular; IEA.

DR GO:0016329; F:apoptosis regulator activity; IEA.
 DR GO:0006915; P:apoptosis; IEA.
 DR InterPro: IPR001315; CARD.
 DR InterPro: IPR004020; PAAD_DAPIN_dom.
 DR Pfam: PF02758; PAAD_DAPIN7; 1.
 DR PROSITE: PS50209; CARD; 1.
 DR PROSITE: PS50824; DAPIN; 1.
 SQ SEQUENCE 195 AA; 21917 MW; 7C9D4BD8DA9A9E8 CRC64;

Query Match 48.6%; Score 238; DB 6; Length 195;
 Best Local Similarity 58.0%; Pred. No. 7.7e-17;
 Matches 47; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 LHFVDQYREQLIARTVTSVEVLDKLGQVLSQEQYERVLAEINTPPSQMRKLFSLSQSWDR 60
 DB 112 LHFVDQYREQLIARTVTSVEVLDKLGQVLSQEQYERVLAEINTPPSQMRKLFSLSQSWDR 171

QY 61 KCKDGLYQALKETHPHLIMEL 81
 DB 172 TKCLLLQALRDTQPYLVDDL 192

RESULT 2
 Q8CHK8 PRELIMINARY; PRT; 193 AA.
 AC Q8CHK8
 DT 01-MAR-2003 (TremBLrel. 23, Created)
 DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
 DE Apoptosis-associated speck-like protein.
 GN RASC.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Masumoto J., Zhou W., Chen F.F., Su F., Kuwada J.Y., Hidaka E.,
 RA Katsuyama T., Sagara J., Taniguchi S., Ngo-Hazlett P.,
 RA Postlethwait J.H., Nunez G., Inohara N.;
 RT "Casp-1: A zebrafish caspase activated by ASC oligomerization required
 RT for pharyngeal Arch development.";
 RL J. Biol. Chem. 0:0-0(2002).
 DR EMBL: AB053165; BAC43754.1; -
 DR GO:0005622; C:intracellular; IEA.
 DR GO:0016329; F:apoptosis regulator activity; IEA.
 DR GO:0006915; P:apoptosis; IEA.
 DR InterPro: IPR001315; CARD.
 DR Pfam: PF02758; PAAD_DAPIN; 1.
 DR PROSITE: PS50209; CARD; 1.
 DR PROSITE: PS50824; DAPIN; 1.
 SQ SEQUENCE 193 AA; 21654 MW; F3B27B56D86A17B CRC64;

Query Match 42.9%; Score 210; DB 11; Length 193;
 Best Local Similarity 48.8%; Pred. No. 6.2e-14;
 Matches 39; Conservative 20; Mismatches 21; Indels 0; Gaps 0;

QY 2 HFVDQYREQLIARTVTSVEVLDKLGQVLSQEQYERVLAEINTPPSQMRKLFSLSQSWDRK 61
 DB 111 HFVDQYREQLIARTVTSVEVLDKLGQVLSQEQYERVLAEINTPPSQMRKLFSLSQSWDRK 170

QY 62 KCKDGLYQALKETHPHLIMEL 81
 DB 171 CKNLFLEALRDTQPYLVDDL 190

RESULT 3
 Q8XNW6 PRELIMINARY; PRT; 1175 AA.
 AC Q8XNW6
 DT 01-MAR-2002 (TremBLrel. 20, Created)
 DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)

DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
 DE Probable exonuclease.
 GN SBCC OR CPE0216.
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=13 / Type A;
 EX MEDLINE=21664373; PubMed=11792842;
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
 RT "complete genome sequence of Clostridium perfringens, an anaerobic
 RT flesh-eater.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 DR EMBL: AP003185; BAB79922.1; -
 DR GO:0016020; C:membrane; IEA.
 DR GO:0005524; F:ATP binding; IEA.
 DR GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; IEA.
 DR GO:0004527; F:exonuclease activity; IEA.
 DR GO:0006810; P:transport; IEA.
 DR InterPro: IPR003439; ABC transporter.
 KW Exonuclease; Complete proteome.
 SQ SEQUENCE 1175 AA; 136878 MW; 7C6D2366525019C1 CRC64;

Query Match 17.2%; Score 84.5; DB 16; Length 1175;
 Best Local Similarity 26.1%; Pred. No. 5.7;
 Matches 24; Conservative 26; Mismatches 31; Indels 11; Gaps 3;

QY 4 VDOYREQLIARTVTSVEVLDKLGQVLSQEQYERVLAEINTPPSQMRKLFSLSQSWDR 55
 DB 924 IEYDNVLIKKANIELLIKKLNGSLFEETWVLOKQNTKELKEVEELKRLVTES 983

QY 56 QSWDRKC---KDGLYQALKETHPHLIMELWEK 84
 DB 984 ESIKKKLEQRDLIHAKQEHKLLALSDLEK 1015

RESULT 4
 Q8EN79 PRELIMINARY; PRT; 614 AA.
 AC Q8EN79
 DT 01-MAR-2003 (TremBLrel. 23, Created)
 DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
 DE Asparagine synthetase (EC 6.3.5.4).
 GN O82608.
 OS Oceanobacillus theyensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
 OX NCBI_TaxID=182710;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HT831 / DSM 14371 / JCM 11309;
 RX MEDLINE=22220767; PubMed=12235376;
 RA Takami H., Takaki Y., Uchiyama I.;
 RT "Genome sequence of Oceanobacillus theyensis isolated from the Iheya
 RT Ridge and its unexpected adaptive capabilities to extreme
 RT environments.";
 RL Nucleic Acids Res. 30:3927-3935(2002).
 DR EMBL: AF004601; BAC14584.1; -
 DR GO:0004066; F:asparagine synthase (glutamine-hydrolyzing) . .; IEA.
 DR GO:0016874; F:Ligase activity; IEA.
 DR GO:0006529; P:asparagine biosynthesis; IEA.
 DR GO:0008152; P:metabolism; IEA.
 DR InterPro: IPR001962; Asn_synthase.
 DR InterPro: IPR006426; Asn_synth_AEB.
 DR InterPro: IPR00583; GATase_2.
 DR Pfam: PF00733; Asn_synthase; 1.
 DR Pfam: PF00310; GATase_2; 1.
 DR TIGRFAMs: TIGR01536; asn_synth_AEB; 1.
 KW Ligase; Complete proteome.
 SQ SEQUENCE 614 AA; 70516 MW; 739525F8CA2B94F1 CRC64;

Query Match	16.8%;	Score 82.5;	DB 16;	Length 614;
Best Local Similarity	26.4%;	Pred. No. 4.3;		
Matches	29;	Conservative	20;	Mismatches 28; Indels 33; Gaps 6

QY	15	VTSVEVLDKLGH-----QVLSQEQYERVLAEINTR-----PSQMRKLFSLSQSW- 58
DB	404	IRSLSDRIDLLHGDKWKKLLDLESTVQSQYQSTIAETPRLDGDKIDAKRELFYLNQWF 463
QY	59	-----DRKCKDGLYQALKETHP---HLIMEL-----WE-----KGSKKGLL 91
DB	464	MSQLLDKDRMSMGASLEVRVPFADHRLVEYVWNIPWDIKWVNGHEKGIL 513

RESULT 5	
Q8GBV1	
ID	Q8GBV1 PRELIMINARY; PRT; 260 AA.
AC	Q8GBV1;
DT	01-WAR-2003 (TrEMBLrel. 23, Created)
DT	01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Putative transposase (Fragment).
GN	TNPA.
OS	Pseudomonas sp. F12.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC	Pseudomonadaceae; Pseudomonas.
OX	NC81_TaxID=217730;
RN	[1]_TaxID=217730;
RC	SEQUENCE FROM N.A.
RC	STRAIN=F12;
RA	Hill K.E., Weightman A.J.;
RT	"Horizontal transfer of dehalogenase genes on IncP-beta plasmids
RT	during bacterial adaptation to degrade alpha-halocarboxylic acids.";
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AJ534880; CAD59131.1; --
DR	GO; GO:0003677; F:DNA binding; IEA.
DR	GO; GO:0004803; F:transposase activity; IEA.
DR	GO; GO:0006310; F:DNA recombination; IEA.
DR	InterPro; IPR002560; Transposase 12.
DR	Pfam; PF01610; Transposase_12; 1.
FT	NON_TER 1
FT	NON_TER 260
SQ	SEQUENCE 260 AA; 30910 MW; 32BC1FA00D6ABF3B CRC64;

Query Match	16.2%;	Score 79.5;	DB 2;	Length 260;
Best Local Similarity	32.1%;	Pred. No. 3.3;		
Matches	27;	Conservative	9;	Mismatches 29; Indels 19; Gaps 4

QY	7	YREQLIARTVSVEVLDKLGQVLSQEQYREV---LAETRPQMRKLFSLSQSWDRCKK 63
DB	146	YRAAKVAKLPQARIVVDKHFVVRWANDALERVKGLRKELKPSQSRTL-----KGRKI- 199
QY	64	DGLYQALKETH-----PHLIMELW 82
DB	200	-----LLKFAHEVSDRERLIMETW 218.

RESULT 6	
Q8G977	
ID	Q8G977 PRELIMINARY; PRT; 260 AA.
AC	Q8G977;
DT	01-WAR-2003 (TrEMBLrel. 23, Created)
DT	01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Putative transposase (Fragment).
GN	TNPA.
OS	Pseudomonas putida.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC	Pseudomonadaceae; Pseudomonas.
OX	NC81_TaxID=303;
RN	[1]
RC	SEQUENCE FROM N.A.
RC	STRAIN=PP3;

SQ SEQUENCE 404 AA; 47498 MW; 2B130E43026E5404 CRC64;

Query Match 16.2%; Score 79.5; DB 2; Length 404;
Best Local Similarity 32.1%; Pred.No.5.8;
Matches 27; Conservative 9; Mismatches 29; Indels 19; Gaps 4

QY 7 YREQLIARTVSEVVVLKLGHVLSQSQYERV--LAENTRPSQMRKLFSLSSQSWDRCK 63
||| : : : : : ||| : : : : : ||| : : : : :
Db 186 YRAAVKAVLPQARIVVDKFHVRMANDALERVKRGKLKFSQSRTL-----KGDKKI- 239

QY 64 DGLYOALKETH-----PHLIMELW 82
||| : : : : : ||| : : : : :
Db 240 -----LLKRAHEVSDRRERLIMETW 258

RESULT 9
Q9X7J2 PRELIMINARY; PRT; 425 AA.

ID Q9X7J2 AC Q9X7J2;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Putative transposase.
OS Pseudomonas stutzeri (Pseudomonas perfectomarina).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
CC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=316;
RN [1]_TaxID=316;
RP SEQUENCE FROM N.A.
RC STRAIN=M1;
RX MEDLINE=99240403; PubMed=10223973;
RA Bolognese F., Di Lecce C., Galli E., Barbieri P.;
RT "Activation and inactivation of Pseudomonas stutzeri methylbenzene
catabolism pathways mediated by a transposable element.";
RL Appl. Environ. Microbiol. 65:1876-1882(1999).
DR EMU; A012352; CAB42636.1; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004803; F:transposase activity; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR InterPro; IPR002560; Transposase 12.
DR Pfam; PF01610; Transposase 12; I-
SQ SEQUENCE 425 AA; 49494 MW; 4EE338A74655B6BF CRC64;

Query Match 16.2%; Score 79.5; DB 2; Length 425;
Best Local Similarity 32.1%; Pred.No.5.8;
Matches 27; Conservative 9; Mismatches 29; Indels 19; Gaps 4

QY 7 YREQLIARTVSEVVVLKLGHVLSQSQYERV--LAENTRPSQMRKLFSLSSQSWDRCK 63
||| : : : : : ||| : : : : : ||| : : : : :
Db 207 YRAAVKAVLPQARIVVDKFHVRMANDALERVKRGKLKFSQSRTL-----KGDKKI- 260

QY 64 DGLYOALKETH-----PHLIMELW 82
||| : : : : : ||| : : : : :
Db 261 -----LLKRAHEVSDRRERLIMETW 279

RESULT 10
Q8ZSQ2 PRELIMINARY; PRT; 193 AA.

ID Q8ZSQ2 AC Q8ZSQ2;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Hypothetical protein PAE3635.
GN PAE3635.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX MEDLINE=21664397; PubMed=11792869;

[illegible]

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RA Montaguelli X., Ceccaidi P.E., Deubel V., Guenet J.L., Despres P.;
RT "A nonsense mutation in the gene encoding 2'-5'-oligoadenylate
RT synthetase/L1 isoform is associated with West Nile virus
RT susceptibility in laboratory mice."
RL Proc. Natl. Acad. Sci. U.S.A. 99:11311-11316(2002).
DR EMBL; BC012877; AAH12877.1; -
DR EMBL; AF466823; AAM37604.1; -
DR MGD; MGI:2180860; Oasla.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005723; F:RNA binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006117; 2SA_SYNTH_2.
DR InterPro; IPR006116; 2SA_SYNTH_US.
DR InterPro; IPR001201; PAP_2SA_core.
DR PROSITE; PS00833; 2SA_SYNTH_2; 1.
DR PROSITE; PS0152; 2SA_SYNTH_3; 1.
DR PROSITE; PS0152; 2SA_SYNTH_3; 1.
SQ SEQUENCE 376 AA; 43934 MW; 30F970452408FB7E CRC64;

Query Match 15.8%; Score 77.5; DB 11; Length 376;
Best Local Similarity 28.3%; Pred. No. 8.2; Mismatches 40; Indels 9; Gaps 3;
Matches 26; Conservative 17;

QY 1 LHFVDQREQLIARTVTSVEVLDLKHGVLSQEQYERVLAEINTRPSQMRKLFSLSSQMDR 60
DB 155 LNILKKNQQYANLISGRTEPLGR-EGKLLTCFNGLRKYFLNCFPTKRLHLHVTHWYQ 213
QY 61 KCKDGLVQALKETHPHLIMEL-----WEKSK 87
DB 214 LCKEKLGDPLP---FOVALELLTYAWEYGSR 242

RESULT 14
Q95Q18 PRELIMINARY; PRT; 295 AA.
AC Q95Q18;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Y53F4B.39 protein.
GN Y53F4B.39
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Smye R.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; AL132949; CAB61094.1; -
DR WormPep; Y53F4B.39; CE24418.
DR InterPro; IPR001279; Blactamase-like.
DR Pfam; PF00753; lactamase B; 1.
DR SEQUENCE 295 AA; 33102 MW; 5D798FC5C67B97CE CRC64;

Query Match 15.5%; Score 76; DB 5; Length 295;
Best Local Similarity 26.7%; Pred. No. 8.8;
Matches 23; Conservative 17; Mismatches 40; Indels 6; Gaps 2;

QY 4 VDOYREQLIARTVTSVEVLDLKHGVLSQEQYERVLAEINTRPSQMRKLFSLSSQMDRCK 63
DB 206 VDEIEHMKREERIIKVL-KEHEITSMVDVTNQVIADSPWAVLALNNVKLVLKICK 264
QY 64 DGLYQALKETHPHLIMELWEKSKG 89.
DB 265 DGVE-----NPHFTFKWIGGSSG 285

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RESULT 15

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Q8YKJ7 PRELIMINARY; PRT; 482 AA.
AC Q8YKJ7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein ALR7298.
GN ALR7298.
OS Anabaena sp. (strain PCC 7120).
OG Plasmid pCC7120alpha.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpō S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003600; BAB78382.1; -
DR FIR; AB2515; AB2515.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015428; F:type I protein secretor activity; IEA.
DR GO; GO:0009306; P:protein secretion; IEA.
DR InterPro; IPR003997; RtxD.
DR PRINTS; PR01490; RTXTOXIND.
KW Plasmid; Hypothetical protein; Complete proteome.
SQ SEQUENCE 482 AA; 54120 MW; 95E4C016A4FCF66A CRC64;

Query Match 15.3%; Score 75; DB 16; Length 482;
Best Local Similarity 24.1%; Pred. No. 20;
Matches 21; Conservative 21; Mismatches 35; Indels 10; Gaps 3;

QY 15 VTSVEVLDLKHGVLSQEQYERVLAEINTRPSQMRKLFSLSSQMDRCKDGLYQALKETH 74
DB 258 ITQINAELEKLNTRSKQLEQ-NNLAADNTENNQIQEIQQAIARWEKEVDN--STIKSH 314
QY 75 PHLMEL-----WEKSKGKGLPLS 94
DB 315 AGCIVEITATLQYLSPGNRLGTQIS 341

Search completed: July 28, 2004, 08:54:45
Job time : 39.7711 secs

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OM protein - protein search, using sw model

Run on: July 28, 2004, 08:46:37 ; Search time 9.15663 Seconds

(without alignments)
540.228 Million cell updates/sec

Title: US-09-996-617-2_COPY_1335_1429

Perfect score: 490
Sequence: 1 LHFVQYREQLIARVTSVEV.....HLIMELWEKSGKGLPLSS 95

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	490	100.0	1473	1	NAL1_HUMAN
2	253	51.6	193	1	ASC_MOUSE
3	236	48.2	195	1	ASC_HUMAN
4	96	19.6	203	1	ASC_BRARE
5	94.5	19.3	431	1	CARG_HUMAN
6	75	15.3	349	1	OAS1_PIG
7	73.5	15.0	1260	1	LINI_NYCCO
8	72	14.7	953	1	CAR4_HUMAN
9	72	14.7	953	1	CAR4_MOUSE
10	72	14.7	1087	1	OAS3_HUMAN
11	71	14.5	833	1	SVL_STRPN
12	70	14.3	192	1	OASB_MOUSE
13	70	14.3	494	1	ENP2_CHICK
14	69.5	14.2	400	1	OAS1_HUMAN
15	69	14.1	833	1	SVL_STRR6
16	68	13.9	1034	1	BGAL_BACME
17	67.5	13.8	204	1	VNSC_PIIHB
18	67.5	13.8	204	1	VNSC_PIIHE
19	67.5	13.8	344	1	FLIG_BOREU
20	66.5	13.6	200	1	VIP_CHICK
21	66.5	13.6	468	1	SYE_TTHETH
22	66	13.5	455	1	ZFR1_CAEEL
23	66	13.5	804	1	SVL_STAAM
24	66	13.5	807	1	SVL_STAAM
25	66	13.5	833	1	SVL_STRP8
26	65.5	13.4	322	1	VOJA_BACSU
27	65.5	13.4	430	1	ACDL_PIG
28	65.5	13.4	1102	1	MYSC_CHICK
29	65	13.3	358	1	OAS1_RAT
30	65	13.3	454	1	CSP2_MOUSE
31	65	13.3	779	1	PHK2_RHIME
32	65	13.3	1242	1	NPHN_MOUSE
33	64.5	13.2	430	1	ACDL_HUMAN

34 64 13.1 367 1 OASA_MOUSE
35 64 13.1 509 1 AURP_STAAU
36 64 13.1 833 1 SYL_STRMU
37 64 13.1 1182 1 HAIR_MOUSE
38 63.5 13.0 204 1 VNSC_PIIHD
39 63.5 13.0 539 1 RIK2_MOUSE
40 63.5 13.0 611 1 BIR_CHICK
41 63.5 13.0 724 1 P85A_HUMAN
42 63.5 13.0 749 1 SPOT_SPICT
43 63.5 13.0 1178 1 RPOB_TREPA
44 63 12.9 411 1 SYS_CAMJE
45 63 12.9 4466 1 DYHC_ANTCR

ALIGNMENTS

RESULT 1
NAL1_HUMAN
ID NAL1_HUMAN STANDARD; PRT: 1473 AA.
AC Q9C000; Q9BZ29; Q9HAV8; Q9UFT4; Q9Y2E0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE NACHT-, LRR- and PYD-containing protein 2 (Death effector filament-forming ced-4-like apoptosis protein) (Nucleotide-binding domain and caspase recruitment domain) (Caspase recruitment domain protein 7).
DE forming ced-4-like apoptosis protein (Nucleotide-binding domain and caspase recruitment domain) (Caspase recruitment domain protein 7).
GN NALP1 OR DEFCAP OR NAC OR CARD7 OR KIAA0926.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=21169419; PubMed=11270363;
RA Bertin J., D'Stefano P.S.;
RT "The PYRIN domain: a novel motif found in apoptosis and inflammation proteins.";
RL Cell Death Differ. 7:1273-1274(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=21148093; PubMed=11250163;
RA Martinon F., Hofmann K., Ischopp J.;
RT "The pyrin domain: a possible member of the death domain-fold family implicated in apoptosis and inflammation.";
RL Curr. Biol. 11:R118-R120(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Erythrocytopenia;
RX MEDLINE=21153743; PubMed=11076957;
RA Hlaing T., Guo R.-F., Dilley K.A., Loussia J.M., Morrish T.A., Shi M.M., Vincenz C., Ward P.A.;
RT "Molecular cloning and characterization of DEFCAP-L and -S, two isoforms of a novel member of the mammalian Ced-4 family of apoptosis proteins.";
RL J. Biol. Chem. 276:9230-9238(2001).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4), AND PROTEIN INTERACTION.
RC TISSUE=T-cell;
RX MEDLINE=21153744; PubMed=11131115;
RA Chu Z.-L., Pio F., Xie Z., Welsh K., Krajewska M., Krajewski S., Godzik A., Reed J.C.;
RT "A novel enhancer of the Apaf1 apoptosome involved in cytochrome c-dependent caspase activation and apoptosis.";
RL J. Biol. Chem. 276:9239-9245(2001).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX MEDLINE=9946063; PubMed=10231032;
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIII. The complete sequences of 100 new cDNA clones from brain which code

RT for large proteins in vitro. ";
 RL DNA Res. 6:63-70(1999).
 RN [6]
 RP SEQUENCE OF 282-1473 FROM N.A. (ISOFORM 1).
 RC TISSUE=Uterus;
 RA Koehrer K., Beyer A., Mewes H.-W., Gassenhuber J., Wiemann S.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Able to form cytoplasmic structures termed death
 CC effector filaments. Enhances APAF1 and cytochrome c-dependent
 CC activation of pro-caspase-9 and consecutive apoptosis. Seems to
 CC bind ATP.
 CC SUBUNIT: Interacts strongly with caspase 2, weakly with caspase 9
 CC and with APAF1 in a cytochrome c-inducible way leading to the
 CC formation of an apoptosome. This interaction may be ATP-dependent.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=4;
 CC Name=1; Synonyms=NAC beta, DEFCAP-L;
 CC IsoId=Q9C000-1; Sequence=Displayed;
 CC Name=2; Synonyms=NAC alpha, DEFCAP-S;
 CC IsoId=Q9C000-2; Sequence=VSP_004327;
 CC Name=3; Synonyms=NAC gamma;
 CC IsoId=Q9C000-3; Sequence=VSP_004326, VSP_004327;
 CC Name=4; Synonyms=NAC delta; VSP_004327;
 CC IsoId=Q9C000-4; Sequence=VSP_004326;
 CC -!- TISSUE SPECIFICITY: Widely expressed. Isoforms 1 and 2 are
 CC expressed in peripheral blood leukocytes, chronic myelogenous
 CC leukemia cell line K-562, followed by thymus, spleen and heart.
 CC Also detected in lung, placenta, small intestine, colon, kidney,
 CC liver and muscle.
 CC -!- SIMILARITY: Contains 1 DAPIN domain.
 CC -!- SIMILARITY: Contains 1 NACHT domain.
 CC -!- SIMILARITY: Contains 1 CARD domain.
 CC -!- SIMILARITY: Contains 7 leucine-rich (LRR) repeats.
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 CC -----
 DR EMBL; AF298458; AAG15254.1; -
 DR EMBL; AF310105; AAG30286.1; -
 DR EMBL; AF229059; AAK00748.1; -
 DR EMBL; AF229060; AAK00749.1; -
 DR EMBL; AF229061; AAK00750.1; -
 DR EMBL; AF229062; AAK00751.1; -
 DR EMBL; AB023143; BAA76770.1; -
 DR EMBL; AL117470; CAB55945.1; -
 DR PIR; T17255; T17255.
 DR HSP; P13489; I44Y.
 DR MIM; 606636; -
 DR GO; GO:0005622; C:intracellular; IC.
 DR GO; GO:0016506; F:apoptosis activator activity; NAS.
 DR GO; GO:0008656; F:caspase activator activity; NAS.
 DR GO; GO:0019839; F:enzyme binding; IPI.
 DR GO; GO:0006913; F:caspase activation; NAS.
 DR GO; GO:0006917; P:induction of apoptosis; NAS.
 DR InterPro; IPR001315; CARD.
 DR InterPro; IPR001767; Disease_resist.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR007091; LRR_Rninh.
 DR InterPro; IPR007111; NACHT_NTPase.
 DR InterPro; IPR004020; PAAD_DAPIN_dom.
 DR Pfam; PF00560; LRR; 2.
 DR Pfam; PF05729; NACHT; 1.
 DR Pfam; PF02758; PAAD_DAPIN; 1.
 DR PRINTS; PR00364; DISEASERIST.
 DR PROSITE; PS50209; CARD; 1.
 DR PROSITE; PS50824; DAPIN; 1.
 DR PROSITE; PS50837; NACHT; 1.

KW Apoptosis; ATP-binding; Leucine-rich repeat; Repeat;
 KM Alternative splicing
 FT DOMAIN 1 92 DAPIN.
 FT DOMAIN 328 637 NACHT.
 FT REPEAT 704 725 LRR 1.
 FT REPEAT 807 830 LRR 2.
 FT REPEAT 864 887 LRR 3.
 FT REPEAT 921 944 LRR 4.
 FT REPEAT 950 973 LRR 5.
 FT REPEAT 1199 1215 LRR 6.
 FT REPEAT 1216 1236 LRR 7.
 FT DOMAIN 1374 1463 CARD.
 FT NP_BIND 334 341 ATP (POTENTIAL).
 FT VARSPPLIC 958 987 Missing (in isoform 3 and isoform 4).
 FT VARSPPLIC 1262 1305 Missing (in isoform 2 and isoform 3).
 FT MUTAGEN 340 340 /FTId=VSP_004327.
 FT MUTAGEN 340 340 K->L: NO EFFECT.
 FT CONFLICT 155 155 L->H (IN REF. 1).
 FT CONFLICT 246 246 L->S (IN REF. 1).
 FT CONFLICT 782 782 T->S (IN REF. 1).
 FT CONFLICT 878 878 T->M (IN REF. 1).
 FT CONFLICT 995 995 T->I (IN REF. 1).
 FT CONFLICT 1119 1119 M->V (IN REF. 1).
 FT CONFLICT 1184 1184 M->V (IN REF. 1 AND 6).
 FT CONFLICT 1241 1241 V->L (IN REF. 1).
 FT CONFLICT 1366 1366 R->C (IN REF. 1).
 SQ SEQUENCE 1473 AA; 165865 MW; 438F0DCE45C2562D CRC64;
 Query Match 100.0%; Score 490; DB 1; Length 1473;
 Best Local Similarity 100.0%; Pred. No. 1.7e-40;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LHFVQVREQLIARTVTSVEVVDKLGQVLSQEQVERVLAENTRPSQWRKLFSLSQSWDR 60
 DB 1379 LHFVQVREQLIARTVTSVEVVDKLGQVLSQEQVERVLAENTRPSQWRKLFSLSQSWDR 1438
 QY 61 KCKDGLYQALKEHPHLMELWEKSGKGLPLSS 95
 DB 1439 KCKDGLYQALKEHPHLMELWEKSGKGLPLSS 1473
 RESULT 2
 ASC_MOUSE STANDARD; PRT; 193 AA.
 ID ASC_MOUSE Q9EPB4; Q9D2W9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Apoptosis-associated speck-like protein containing a CARD (MASC)
 DE (PYCARD).
 GN ASC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 OX [1]_TaxID=10090;
 RN SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Thymus;
 RX MEDLINE=20580347; PubMed=11139337;
 RA Masumoto J., Taniguchi S., Nakayama K., Ayukawa K., Sagara J.;
 RT "Murine ortholog of ASC, a CARD-containing protein, self-associates
 RT and exhibits restricted distribution in developing mouse embryos.";
 RL Exp. Cell Res. 262:128-133(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Breast tumor;
 RA Martinon F., Hofmann K., Tschopp J.;
 RT "Pycard a PYD and CARD containing molecule.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Pancreas, and Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glasi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffalli D., Bojunga N., Carrinci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayaishizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Spatlenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bosak S.A., McSwan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Fulyk S.W.,
RA Villalon D.K., Murzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Promotes caspase-mediated apoptosis. This proapoptotic
activity is mediated predominantly through the activation of
caspase 9 (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Upstream of caspase activation,
a redistribution from the cytoplasm to the aggregates occurs.
These aggregates appear as hollow, perinuclear spherical, ball-like
structures (By similarity).
CC -1- TISSUE SPECIFICITY: Expressed in small intestine, colon, thymus,
spleen, brain, heart, skeletal muscle, kidney, lung and liver.
CC -1- DEVELOPMENTAL STAGE: Strongly expressed at E9.5 day in the
telencephalon, thalamic areas of the diencephalon, heart and
liver.
CC -1- SIMILARITY: Contains 1 DAPIN domain.
CC -1- SIMILARITY: Contains 1 CARD domain.
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CC -----
DR EMBL; AB032249; BAB16609.1; -
DR EMBL; AF310104; AAG30287.1; -
DR EMBL; AK009852; BAB26543.1; -
DR EMBL; AK007742; BAB25229.1; -
DR EMBL; AK018682; BAB31341.1; -

DR EMBL; BC008252; AAH08252.1; -
DR MGD; MGI:1931465; Asc.
DR GO; GO:0005829; C:cytosol; IDA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR004020; PAAD-DAPIN_dom.
DR Pfam; PF02758; PAAD-DAPIN; 1.
DR PROSITE; PSS0209; CARD; 1.
DR PROSITE; PSS0824; DAPIN; 1.
RT Apoptosis; Anti-oncogene.
FT DOMAIN 1 91 DAPIN.
FT CONFLICT 105 193 CARD.
FT CONFLICT 159 159 K -> E (IN REF. 3).
SQ SEQUENCE 193 AA; 21458 MW; 2A4EA40194870B31 CRC64;
Query Match 51.6%; Score 253; DB 1; Length 193;
Best Local Similarity 61.2%; Pred. No. 4.6e-18;
Matches 49; Conservative 11; Mismatches 20; Indels 0; Gaps 0;
QY 2 HFVDQYREQLIARTVTSVEVLDKLHGVLQSQYERYLAENTRPSOMRKLFLSLQSQWDRK 61
DB 111 HFVDQHQAIIARTVEVDGLDGLHGSVLTEGQYQAVRAETTSQDKRKLFSFVPSWNL 170
QY 62 CKDGLYQALKETHPLIMEL 81
DB 171 CKDSLQALKKEIHPYLVMDL 190
RESULT 3
ASC_HUMAN
ID ASC_HUMAN STANDARD; PRT; 195 AA.
AC Q9UFI3; Q96D12; Q9BSZ5; Q9HED0; Q9NXJ8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Apoptosis-associated speck-like protein containing a CARD (hASC)
DE (PYCARD) (target of methylation-induced silencing 1) (Caspase
DE recruitment domain protein 5).
GN ASC OR TMS1 OR CARDS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Leukemia;
RX MEDLINE=20036508; PubMed=10567338;
RA Masumoto J., Taniguchi S., Ayukawa K., Sarvatham H., Kishino T.,
RA Niihara N., Hidaka E., Katsuyama T., Higuchi T., Sagara J.;
RT "ASC, a novel 22-kDa protein, aggregates during apoptosis of human
proneuroleukemic leukemia HL-60 cells.";
RL J. Biol. Chem. 274:33835-33838(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Fibroblast;
RX MEDLINE=20552139; PubMed=11103776;
RA Conway K.E., McConnell B.B., Bowring C.E., Donald C.D., Warren S.T.,
RA Vertino P.M.;
RT "TMS1, a novel proapoptotic caspase recruitment domain protein, is a
target of methylation-induced gene silencing in human breast
cancers.";
RT Cancer Res. 60:6236-6242(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Martinon F., Hofmann K., Tschopp J.;
RT "pYCARD a PYD and CARD containing molecule.";
Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Bertin J.;
RT "CARD5 protein is a CARD/PYRIN family member that is involved in
apoptosis signal transduction.";
Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [5]

RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Colon mucosa;
 RA Watanabe K., Kunagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
 RA Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
 RA Nakamura Y., Isogai T., Sugano S.;
 RT "NEDO human cDNA sequencing project";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 [6]
 RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
 RP TISSUE=Lymph. and Pancreas;
 RC MEDLINE=2238257; PubMed=12477932;
 EX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [7]
 RN FUNCTION, AND SUBCELLULAR LOCATION.
 RP MEDLINE=20552140; PubMed=1103777;
 RX McConnell B.B., Vertino P.M.;
 RA "Activation of a caspase-9-mediated apoptotic pathway by subcellular
 RT redistribution of the novel caspase recruitment domain protein TWS1.";
 RL Cancer Res. 60:6243-6247 (2000).
 CC -!- FUNCTION: Promotes caspase-mediated apoptosis. This proapoptotic
 CC activity is mediated predominantly through the activation of
 CC caspase 9.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Upstream of caspase activation,
 CC a redistribution from the cytoplasm to the aggregates occurs.
 CC These appeared as hollow, perinuclear spherical, ball-like
 CC structures.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=Q9ULZ3-1; Sequence=displayed;
 CC Name=2;
 CC IsoId=Q9ULZ3-2; Sequence=VSP_004119;
 CC Name=3;
 CC IsoId=Q9ULZ3-3; Sequence=VSP_004118;
 CC Note=No experimental confirmation available;
 CC -!- TISSUE SPECIFICITY: Widely expressed at low levels. Detected in
 CC peripheral blood leukocytes, lung, small intestine, spleen,
 CC thymus, colon and at lower levels in placenta, liver and kidney.
 CC Very low expression in skeletal muscle, heart and brain. Detected
 CC in the leukemia cell lines HL-60 and U937, but not in Jurkat T-
 CC cell lymphoma and David Burkitt's lymphoma. Detected in the
 CC melanoma cell line WM93, but not in WM793. Not detected in HeLa
 CC cervical carcinoma cells and Molt 4 lymphocytic leukemia cells.
 CC -!- MISCELLANEOUS: In breast tumorigenesis, methylation-mediated
 CC silencing may affect genes and proteins that act as positive
 CC mediators of cell death.
 CC -!- SIMILARITY: Contains 1 DAPIN domain.
 CC -!- SIMILARITY: Contains 1 CARD domain.
 CC -!- CAUTION: Ref.5 sequence differs from that shown due to a
 CC frameshift in position 4.
 CC -----
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 CC -----
 CC EMBL; AB023416; BAA87339.2; -;
 CC EMBL; AF184072; AAG01187.1; -;
 CC EMBL; AF184073; AAG01188.1; -;
 CC EMBL; AF255794; AAF99665.1; -;
 CC EMBL; AF310103; AAG30286.1; -;
 CC EMBL; AF384665; AAK63850.1; -;
 CC EMBL; AK000211; BAA91012.1; ALT_FRAME.
 CC EMBL; BC004470; AAH04470.1; -;
 CC EMBL; BC013569; AAH13569.1; ALT_INIT.
 CC MIM; 606838; -;
 CC GO; GO:0006917; P:induction of apoptosis; TAS.
 CC InterPro; IPR001315; CARD.
 CC InterPro; IPR004020; PAAD_DAPIN_dom.
 CC Pfam; PF02758; PAAD_DAPIN; 1.
 CC PROSITE; PS50209; CARD; 1.
 CC PROSITE; PS50824; DAPIN; 1.
 CC KW Apoptosis; Anti-oncogene; Alternative splicing.
 CC FT DOMAIN 1 91
 CC FT DOMAIN 107 195
 CC FT VARSPLIC 26 85
 CC Missing (in isoform 3).
 CC /FTId=VSP_004118.
 CC FT VARSPLIC 93 111
 CC Missing (in isoform 2).
 CC /FTId=VSP_004119.
 CC SQ SEQUENCE 195 AA; 21627 MW; 455987286586F46A CRC64;
 CC Query Match 48.2%; Score 236; DB 1; Length 195;
 CC Best Local Similarity 56.8%; Pred No. 2.2e-16;
 CC Matches 46; Conservative 17; Mismatches 18; Indels 0; Gaps 0;
 CC
 CC QY 1 LHFVDQYREQIARVTSVEVVLKLGQVLSQEQYERVLAEPTPSQMRKLFSLQSWDR 60
 CC DB 112 LHFIDQHRALIAITVNVVLLDLYGKVLTDQVQVRAVPTNPSPKMRKLFSTPAWN 171
 CC QY 61 KKDGLYQALKETHPHLIMEL 81
 CC DB 172 TKDLILQALRESQSYLVEDL 192
 CC
 CC RESULT 4
 CC ASC_BEARE STANDARD; PRT; 203 AA.
 CC ID ASC_BRARE
 CC AC Q919N6;
 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE Apoptosis-associated speck-like protein containing a CARD (PYCARD).
 CC GN ASC OR ASCI.
 CC OS Brachydanio rerio (Zebrafish) (Danio rerio).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 CC OC Cyprinidae; Danio.
 CC OX NCBI_TaxID=7955;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=20373792; PubMed=10917738;
 CC RA Inohara N., Nunez G.;
 CC RT "Genes with homology to mammalian apoptosis regulators identified in
 CC Zebrafish.";
 CC RL Cell Death Differ. 7:509-510 (2000).
 CC -!- FUNCTION: Promotes caspase-mediated apoptosis (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Contains 1 DAPIN domain.
 CC -!- SIMILARITY: Contains 1 CARD domain.
 CC -----
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FT CONFLICT 422 422 L -> P (IN REF. 5).
SQ SEQUENCE 431 AA; 48932 MW; C554D13080773256 CRC64;

Query Match 19.3%; Score 94.5; DB 1; Length 431;
Best Local Similarity 32.5%; Pred. No. 0.05;
Matches 26; Conservative 17; Mismatches 36; Indels 1; Gaps 1;

QY 3 FVDQYREQLIARVTSVEVLDKLH-GQVLSQEQYERVLAEINTRPSQMRKLFSLQSQWDRK 61
DB 347 PVKENHRQLQRMGLDKVLDLQDNEVLTENELVEQKTRQSKNEALLSWVEKKGDL 406

QY 62 CKQGLYQALKETHPHLIMEL 81
DB 407 ALDVLFRSISERDPVLVSYL 426

RESULT 6
OAS1_FIG
ID OAS1_FIG STANDARD; PRT; 349 AA.
AC Q29559; 077734;
DT 15-DEC-1998 (Rel. 37, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 2'-5'-oligoadenylate synthetase 1 (SC 2.7.7.-) ((2-5')oligo(A)
DE synthetase 1) (2-5A synthetase 1) (p42 OAS).
GN OAS1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RA Hartmann R.;
RL Thesis (1997), University of Aarhus, Denmark.
RN [2]
RP SEQUENCE OF 1-128 FROM N.A.
RC TISSUE=Small intestine;
RA MEDLINE=96327607; PubMed=8672129;
RX Winteroe A.K., Fredholm M., Davies W.;
RT "Evaluation and characterization of a porcine small intestine cDNA
RT library: analysis of 839 clones.";
RL Mamm. Genome 7:509-517(1996).
CC -!- FUNCTION: MAY PLAY A ROLE IN MEDIATING RESISTANCE TO VIRUS
CC INFECTION, CONTROL OF CELL GROWTH, DIFFERENTIATION, AND APOPTOSIS.
CC -!- CATALYTIC ACTIVITY: Bands double-stranded RNA and polymerizes ATP
CC into PPP(A2'p5'A)N oligomers, which activate the latent RNase L
CC that, when activated, cleaves single-stranded RNAs.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: ASSOCIATED WITH DIFFERENT SUBCELLULAR
CC FRACTIONS SUCH AS MITOCHONDRIAL, NUCLEAR, AND ROUGH/SMOOTH
CC MICROSOMAL FRACTIONS (BY SIMILARITY).
CC -!- SIMILARITY: Belongs to the 2-5A synthetase family.
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DR EMBL; AJ225090; CAA12397.1; -
DR EMBL; F14610; CAA23153.1; ALT_INIT.
DR InterPro; IPR006117; 25A_SYNTH_2.
DR InterPro; IPR006116; 25A_SYNTH_UB.
DR InterPro; IPR001201; PAP_25A_CORE.
DR PROSITE; PS00832; 25A_SYNTH_1; 1.
DR PROSITE; PS00833; 25A_SYNTH_2; 1.
DR PROSITE; PS0152; 25A_SYNTH_3; 1.
DR RNA-binding; Transferase; Nucleosidyltransferase;
KW Interferon induction.
FT CONFLICT 54 54 V -> F (IN REF. 2).

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FT CONFLICT 122 122 S -> R (IN REF. 2).
SQ SEQUENCE 349 AA; 40246 MW; 06949A35BFCF7710 CRC64;

Query Match 15.3%; Score 75; DB 1; Length 349;
Best Local Similarity 32.7%; Pred. No. 3.3;
Matches 18; Conservative 9; Mismatches 10; Indels 18; Gaps 3;

QY 44 RPSQMRKLFSLQSQWDRKCKDGLYQALKETH-----PHLIMEL-----WEKGSKK 88
DB 200 RPTLKSILRLVKHW-----YTCCKTHGNKLPPOYALELLTVYAWEGSSRK 246

RESULT 7
LIN1_NYCCO
ID LIN1_NYCCO STANDARD; PRT; 1260 AA.
AC P08548;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-AUG-1988 (Rel. 08, Last annotation update)
DE LINE-1 reverse transcriptase homolog.
OS Nycticebus coucang (Slow loris).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Loridae; Nycticebus.
OX NCBI_TaxID=9470;
RN [1]
RP SEQUENCE.
RX MEDLINE=86230917; PubMed=2423883;
RA Hattori M., Kuhara S., Takenaka O., Sakaki Y.;
RT "L1 family of repetitive DNA sequences in primates may be derived
RT from a sequence encoding a reverse transcriptase-related protein.";
RL Nature 321:625-628(1986).
CC -!- MISCELLANEOUS: THIS SEQUENCE WAS CONSTRUCTED FROM AN ALIGNMENT OF
CC SIX SEQUENCES, DETERMINED BY THESE AUTHORS BUT NOT SHOWN,
CC BELONGING TO THE LINE-1 FAMILY.
CC PIR; B25313; GNLR1.
CC DR HSP; P27695; 1HD7.
CC DR InterPro; IPR005135; Exo_endo_phos.
CC DR InterPro; IPR000477; RVTse.
CC DR Pfam; PF03372; Exo_endo_phos; 1.
CC DR Pfam; PF00078; rvt; 1.
CC DR RNA-directed DNA polymerase.
CC KW RNA-directed DNA polymerase.
CC SQ SEQUENCE 1260 AA; 147042 MW; 7A6803DF471F7253 CRC64;

Query Match 15.0%; Score 73.5; DB 1; Length 1260;
Best Local Similarity 23.0%; Pred. No. 19;
Matches 23; Conservative 24; Mismatches 38; Indels 15; Gaps 3;

QY 4 VDQYREQLIA-----RVTSEVVDKLHQVLSQEQYERVLAEINTRPSQMRKLFSLQSQW 59
DB 410 LNEYKLYSHKYENLKEIDQVLEACHLPRLSQKEVEML---NRPISSEIASTIQNLP 465

QY 60 RKCKDG-----LYQALKETHPHLIMELWEKGSKKGLLP 92
DB 466 KKKSPDPGTFSEFYQTFRBELVPILLNFQNIEREGILP 505

RESULT 8
CAR4_HUMAN
ID CAR4_HUMAN STANDARD; PRT; 953 AA.
AC Q9Y239; Q8IWF5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caspase recruitment domain protein 4 (Nod1 protein).
GN CAR4 OR NOD1.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endothelial cells;
RX MEDLINE=99240667; PubMed=10224040;

```


RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Wu Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT ALA-884.
RC STRAIN=Czech II, and FVB/N; TISSUE=Breast cancer;
RX MEDLINE=2238257; PubMed=12477932;
RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Collins F.S., Wagner L., Shenmer C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J.J., Helton E., Kettunen M., Madan A.A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Matra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Enhances caspase-9-mediated apoptosis. Induces NF-kappa-
B activity via RICK (CARDIAC, RIP2) and IKK-gamma. Confers
responsiveness to intracellular bacterial lipopolysaccharides
(LPS) (By similarity).
CC -!- SUBUNIT: Self-associates. Binds to caspase-9 and RICK by CARD-CARD
interaction (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Contains 1 CARD domain.
CC -!- SIMILARITY: Contains 1 NACHT domain.
CC -!- SIMILARITY: Contains 9 leucine-rich (LRR) repeats.
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CC -----
DR EMBL; AK082663; BAC38566.1; -
DR EMBL; AK089662; BAC40940.1; -
DR EMBL; BC042670; AAH42670.1; -
DR EMBL; BC043670; AAH43670.1; -
DR MGD; MGI:1341839; Card4.
DR InterPro; IPR001315; LRR.
DR InterPro; IPR007091; LRR_Ninh.
DR InterPro; IPR007111; NACHT_NTFase.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF05729; NACHT; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS50837; NACHT; 1.
KW Apoptosis; ATP-binding; Repeat; Leucine-rich repeat; Polymorphism.
FT DOMAIN 15 107 CARD.
FT DOMAIN 196 531 NACHT.

FT NP_BIND 202 209 ATP (POTENTIAL).
FT REPEAT 17 42 LRR 1.
FT REPEAT 702 725 LRR 2.
FT REPEAT 727 750 LRR 3.
FT REPEAT 755 778 LRR 4.
FT REPEAT 783 806 LRR 5.
FT REPEAT 839 862 LRR 6.
FT REPEAT 867 890 LRR 7.
FT REPEAT 895 918 LRR 8.
FT REPEAT 923 946 LRR 9.
FT VARIANT 884 884 S -> A (in strain Czech II).
SQ SEQUENCE 953 AA; 107739 MW; 39C639621C8B1A58 CRC64;
Query Match 14.7%; Score 72; DB 1; Length 953;
Best Local Similarity 26.0%; Pred. No. 20;
Matches 20; Conservative 17; Mismatches 38; Indels 2; Gaps 2;
QY 8 REQLIARVTSVEVLDK-LHGQVLSCEQYERVLAEINTPSQWRKLFSLSQSWDRCKDGL 66
DB ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
27 REHLVTNIRNTQCLVDNLENGYFSAEDAIEIVCACTPKDKVRKILLDLVQSGKEVSEFF 86
QY 67 YQALXETH-PLHIMELW 82
DB ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
87 LVVLOQLDEAYVDLRW 103
RESULT 10
OAS3 HUMAN STANDARD; PRT; 1087 AA.
ID -OAS3 HUMAN
AC Q9Y6K5; OGH3P5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 10-OCT-2001 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 2'-5'-oligoadenylate synthetase 3 (EC 2.7.7.-) (2-5')oligo(A)
DE synthetase 3) (2-5A synthetase 3) (p100 OAS) (P/OAKL.4).
GN OAS3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=9909899; PubMed=9880533;
RA Rebouillat D., Hovnanian A., Marie I., Hovanesian A.G.;
RT "The 100-kDa 2',5'-oligoadenylate synthetase catalyzing preferentially
the synthesis of dimeric pppA2'p5'A molecules is composed of three
homologous domains";
RL J. Biol. Chem. 274:1557-1565(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21174977; PubMed=11280764;
RA Ito M., Shichijo S., Tsuda N., Ochi M., Harashima N., Saito N.,
RA Itoh K.;
RT "Molecular basis of T cell-mediated recognition of pancreatic cancer
cells";
RL Cancer Res. 61:2038-2046(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA Muzny D., Arenson A.D., Adams C., Bunac C., Carvelli K., Chang J.,
RA Chacko J., Chen J., Ding Y., Dugan S., Durbin J., Forcum J.,
RA Ganesh R., Garcia C., Goodman M., Gorrell J.H., Haywood M.,
RA Hernandez J., Jackson L., Jin S., Kampal R., Karpthy S., Kovar C.,
RA Lau S., Leal B., Lee E., Li Y., Lichtarge O., Liu W., Logan O., Lu J.,
RA Ly T., Marondel I., Martinez C., Merscher K., Montgomery K., Oswal G.,
RA Perez L., Rashid N.D., Renault B., Rowland K., Savage L.,
RA Scherer S.E., Shen H., Simon M., Stovall K., Timms K.M., Todd J.,
RA Gibb R.A.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-59 FROM N.A.
RC TISSUE=Monocytes;
RX MEDLINE=20564207; PubMed=11112351;

Reboullat D., Hovnanian A., David G., Hovanessian A.G.,
Williams B.R.;
RT "Characterization of the gene encoding the 100-kDa form of human 2',
RT 5'-oligoadenylate synthetase";
RL Genomics 70:232-240(2000).
CC -!- FUNCTION: MAY PLAY A ROLE IN MEDIATING RESISTANCE TO VIRUS
CC INFECTION, CONTROL OF CELL GROWTH, DIFFERENTIATION, AND APOPTOSIS.
CC OAS3 SYNTHESIZES PREFERENTIALLY DIMERIC 2',5'-OLIGADENYLATE
CC MOLECULES. GTP CAN BE AN ALTERNATIVE SUBSTRATE.
CC -!- CATALYTIC ACTIVITY: Binds double-stranded RNA and polymerizes ATP
CC into pPP(A2'P5'A')N oligomers, which activate the latent RNase L
CC that, when activated, cleaves single-stranded RNAs.
CC -!- SUBUNIT: Monomer.
CC -!- TISSUE SPECIFICITY: PRESENT AT HIGH LEVEL IN PLACENTA TROPHOBLAST.
CC -!- INDUCTION: By interferons.
CC -!- SIMILARITY: Belongs to the 2-5A synthetase family.

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DR EMBL; AF063613; AXD28543.1; -;
DR EMBL; AF044545; BAB18647.1; -;
DR EMBL; AQ004531; -; NOT_ANNOTATED_CDS.
DR EMBL; AR251351; -; NOT_ANNOTATED_CDS.
DR Genew; HGNC:8088; OAS3.
DR MIM; 603351; -;
DR GO; GO:0005792; C:microsome; TAS.
DR GO; GO:0006139; P:nucleobase, nucleoside, and nucl. . .; TAS.
DR InterPro; IPR006117; 25A_SYNTH_2.
DR InterPro; IPR006116; 25A_synth_UB.
DR InterPro; IPR002934; NTP_transf.
DR InterPro; IPR001201; PAP_25A_core.
DR Pfam; PFO1909; NTP_transf_2; 1.
DR PROSITE; PS00832; 25A_SYNTH_1; 2.
DR PROSITE; PS00833; 25A_SYNTH_2; 2.
DR PROSITE; PS50152; 25A_SYNTH_3; 3.
KW RNA-binding; Transferase; Nucleosidytransferase; Repeat;
KW Interferon induction.
KW DOMAIN 6 343 OAS DOMAIN 1.
FT DOMAIN 344 410 LINKER.
FT DOMAIN 411 742 OAS DOMAIN 2.
FT DOMAIN 750 1084 OAS DOMAIN 3.
FT CONFLICT 18 18 R->K (IN REF. 2).
FT CONFLICT 159 159 G->A (IN REF. 1).
FT CONFLICT 249 249 A->G (IN REF. 1).
FT CONFLICT 287 288 QL->HV (IN REF. 1).
FT CONFLICT 316 316 L->H (IN REF. 1).
FT CONFLICT 393 398 GAASIV->AEPASY (IN REF. 1).
FT CONFLICT 503 504 HV->QL (IN REF. 3).
FT CONFLICT 984 984 G->R (IN REF. 2).
SQ SEQUENCE 1087 AA; 121164 MW; 3DABED08FB08AEB CRC64;

Query Match 14.7%; Score 72; DB 1; Length 1087;
Best Local Similarity 35.0%; Pred. No. 23;
Matches 21; Conservative

QY 42 NITRPSQWRKLFPSISQSW-DRKKCDGLYQALKETHPHL-IMEL-----WEGSKGLPLS 94
DB 193 NIRPAKLNILLVKWHYQVCLQGLW---KETLPPYALLELTTFWAEQCKKDAFSLA 249

RESULT 11
SYL_STRPN
ID_SYL_STRPN STANDARD; PRT; 833 AA.
AC Q97SS0;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE 2'-5'-oligoadenylate synthetase 1B (EC 2.7.7.-) ((2-5')oligo(A)
 DE synthetase 1B) (2-5A synthetase 1B) (Fragment).
 GN OAS1B OR OIAS2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91232962; PubMed=1709495;
 RA Rutherford M.N., Kumar A., Nessim A., Chebath J., Williams B.R.G.;
 RT "The murine 2-5A synthetase locus: three distinct transcripts from two
 RT linked genes".
 RL Nucleic Acids Res. 19:1917-1924(1991).
 CC -!- FUNCTION: THE 2-5A SYSTEM (THE OASs, 2-5A, AND RNASE L) MAY PLAY A
 CC ROLE IN MEDIATING RESISTANCE TO VIRUS INFECTION, CONTROL OF CELL
 CC GROWTH, DIFFERENTIATION, AND APOPTOSIS.
 CC -!- CATALYTIC ACTIVITY: Binds double-stranded RNA and polymerizes ATP
 CC into ppp(A2'p5'A)n oligomers, which activate the latent RNase L
 CC that, when activated, cleaves single-stranded RNAs.
 CC -!- INDUCTION: By interferons.
 CC -!- SIMILARITY: Belongs to the 2-5A synthetase family.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC
 DR EMBL; X55982; CAA39455.1; -.
 DR PIR; S15661; S15661.
 DR MGI; MGI:97430; Oas1b.
 DR GO; GO:0003800; Oas1b.
 DR InterPro; IPR006117; 2SA_SYNTH_2.
 DR InterPro; IPR006116; 2SA_SYNTH_UB.
 DR InterPro; IPR001201; PAP_2SA_core.
 DR PROSITE; PS00832; 2SA_SYNTH_1; PARTIAL.
 DR PROSITE; PS00833; 2SA_SYNTH_2; PARTIAL.
 DR PROSITE; PS50152; 2SA_SYNTH_3; 1.
 KW RNA-binding; Transferase; Nucleotidyltransferase;
 KW Interferon induction.
 FT NON TER 1
 FT NON TER 192
 FT NON TER 192 192
 SQ SEQUENCE 192 AA; 21936 MW; 4E1C011BF9024F46 CRC64;
 Query Match 14.3%; Score 70; DB 1; Length 192;
 Best Local Similarity 33.3%; Pred. No. 5.4; Indels 8; Gaps 2;
 Matches 17; Conservative 9; Mismatches 17; Indels 8; Gaps 2;
 QY 42 NTRPSQMRKFLSLSQSWDRKCKGLGYQALKETHPHLIMEL-----WEKGSK 87
 DB 137 NCRPTKLRLRLVTHVYQLCKELGDPPL--PQVALELLTLDAWEYGSK 184
 RESULT 13
 ENP2 CHICK
 ID ENP2_CHICK STANDARD; PRT; 494 AA.
 AC P79784;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ectonucleoside triphosphate diphosphohydrolase 2 (EC 3.6.1.3)
 DE (NTPDase2) (ecto-ATPase) (CD39 antigen-like 1).
 GN ENTPD2 OR CD39L1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-21; 68-73; 83-90; 108; 121;

RP 144-150; 154-176; 208-217; 251-258; 273-284; 337-352; 374-380;
 RP 383-389; 448-456 AND 459-479.
 RC TISSUE=Gizzard, and Skeletal muscle;
 RX MEDLINE=97150869; PubMed=8995405;
 RA Kirley T.L.;
 RT "Complementary DNA cloning and sequencing of the chicken muscle ecto-
 RT ATPase. Homology with the lymphoid cell activation antigen CD39.";
 RL J. Biol. Chem. 272:1076-1081(1997).
 RN [2]
 RP SEQUENCE OF 1-12 AND 154-176, AND CHARACTERIZATION.
 RX MEDLINE=95081479; PubMed=7989647;
 RA Stout J.G., Kirley T.L.;
 RT "Purification and characterization of the ecto-Mg-ATPase of chicken
 RT gizzard smooth muscle.";
 RL J. Biochem. Biophys. Methods 29:61-75(1994).
 CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other
 CC nucleotides to regulate purinergic neurotransmission. Hydrolyzes
 CC ADP only to a marginal extent (By similarity).
 CC -!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
 CC -!- COFACTOR: Requires calcium and magnesium.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- PTM: Has probably disulfide bonds.
 CC -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC
 DR EMBL; U74467; AAC60071.1; -.
 DR InterPro; IPR000407; GDA1_CD39_NTPase.
 DR Pfam; PF01150; GDA1_CD39_1.
 DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
 KW Hydrolyase; Transmembrane; Glycoprotein; Calcium; Magnesium.
 FT INIT MET 0 0
 FT DOMAIN 1 3
 FT DOMAIN 1 3
 FT TRANSMEM 4 24
 FT DOMAIN 25 464
 FT TRANSMEM 465 485
 FT DOMAIN 486 494
 FT DOMAIN 8 13
 FT CARBOHYD 61 61
 FT CARBOHYD 296 296
 FT CARBOHYD 417 417
 FT CARBOHYD 443 443
 FT CONFLICT 11 11
 FT CONFLICT 174 176
 FT CONFLICT 174 176
 SQ SEQUENCE 494 AA; 54402 MW; 1E0E0E631DA621EE CRC64;
 Query Match 14.3%; Score 70; DB 1; Length 494;
 Best Local Similarity 36.4%; Pred. No. 15;
 Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;
 QY 21 VLDKLHGQVLSEQYERVLAEVTRPSQMRKFLSLSQSWDRCKD 64
 DB 244 VLKRLLSKYLAENYQETVANPCWPTGYRKSLSLSSIIYDSPCTE 287
 RESULT 14
 OAS1 HUMAN
 ID OAS1_HUMAN STANDARD; PRT; 400 AA.
 AC P00973; P04820; P29080; P29081; P78485; P78486; Q16700; Q16701;
 AC Q96J61;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-NAR-2004 (Rel. 43, Last annotation update)
 DE 2'-5'-oligoadenylate synthetase 1 (EC 2.7.7.-) ((2-5')oligo(A)
 DE synthetase 1) (2-5A synthetase 1) (p46/p42 OAS) (E18/E16).
 GN OAS1 OR OIAS.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A. (ISOFORMS P41 AND P46).
 RX MEDLINE=86081732; PubMed=2416561;
 RA Benesh P., Mory Y., Revel M., Chebath J.;
 RT "Structure of two forms of the interferon-induced (2'-5') oligo A
 RT synthetase of human cells based on cDNAs and gene sequences.";
 RL EMBO J. 4:2249-2256(1985).
 RN [2]
 RN SEQUENCE FROM N.A. (ISOFORM P41).
 RP MEDLINE=86223945; PubMed=3754863;
 RA Shiojiri S., Fukunaga R., Ichii Y., Sokawa Y.;
 RT "Structure and expression of a cloned cDNA for human (2'-
 RT 5')oligoadenylate synthetase.";
 RL J. Biochem. 99:1455-1464(1986).
 RN [3]
 RN SEQUENCE FROM N.A. (ISOFORM P41).
 RP MEDLINE=86108911; PubMed=3753689;
 RA Watheliet M.G., Moutschen S., Cravador A., Dewit L., Defilippi P.,
 RA Huez G.A., Content J.;
 RT "Full-length sequence and expression of the 42 kDa 2-5A synthetase
 RT induced by human interferon.";
 RL FEBS Lett. 196:113-120(1986).
 RN [4]
 RN SEQUENCE FROM N.A. (ISOFORMS P48 AND P41).
 RP MEDLINE=91332052; PubMed=1651324;
 RA Ghosh S.K., Kusari J., Bandyopadhyay S.K., Samanta H., Kumar R.,
 RA Sen G.C.;
 RT "Cloning, sequencing, and expression of two murine
 RT 2'-5'-oligoadenylate synthetases. Structure-function relationships.";
 RL J. Biol. Chem. 266:15293-15299(1991).
 RN [5]
 RN SEQUENCE FROM N.A.
 RP Muzny D., Arenson A.D., Adams C., Bunac C., Carvelli K., Chang J.,
 RA Chacko J., Chen J., Ding Y., Dugan S., Durbin J., Forcum J.,
 RA Ganesh R., Garcia C., Goodman M., Gortell J.H., Haywood M.,
 RA Hernandez J., Jackson L., Jin S., Kampal R., Karpachy S., Kovar C.,
 RA Lau S., Leal B., Lee E., Li Y., Lichtarge O., Liu W., Logan O., Lu J.,
 RA Ly T., Marondel I., Martinez C., Merscher S., Montgomery K., Oswal G.,
 RA Perez L., Rashid N.D., Renault B., Rowland K., Savage L.,
 RA Scherer S.E., Shen H., Simon M., Stovall K., Timms K.M., Todd J.,
 RA Vo Q., Williamson A., Worley K.C., Yu W., Kucherlapati R., Nelson D.,
 RA Gibbs R.A.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RN SEQUENCE FROM N.A. (ISOFORM P41).
 RP TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RN SEQUENCE OF 255-364 FROM N.A. (ISOFORM P41).
 RP MEDLINE=83273721; PubMed=6348777;

RA Merlin G., Chebath J., Benesh P., Metz R., Revel M.;
 RT "Molecular cloning and sequence of partial cDNA for
 RT interferon-induced (2'-5')oligo(A) synthetase mRNA from human
 RT cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4904-4908(1983).
 RN [8]
 RN SEQUENCE OF 231-400 FROM N.A. (ISOFORM P41), AND INDUCTION.
 RP TISSUE=Lymphoblast;
 RX MEDLINE=85284968; PubMed=2411547;
 RA Saunders M.E., Gewirtz D.R., Fugwell M.E., McMahon M.,
 RA Williams B.R.G.;
 RT "Human 2-5A synthetase: characterization of a novel cDNA and
 RT corresponding gene structure.";
 RL EMBO J. 4:1761-1768(1985).
 RN [9]
 RN SEQUENCE OF 1-28 FROM N.A.
 RP MEDLINE=88082760; PubMed=3121313;
 RA Watheliet M.G., Clausen I.M., Nols C.B., Content J., Huez G.A.;
 RT "New Inducers revealed by the promoter sequence analysis of two
 RT interferon-activated human genes.";
 RL Eur. J. Biochem. 169:313-321(1987).
 RN [10]
 RN SEQUENCE OF 1-27 FROM N.A.
 RP TISSUE=Liver;
 RX MEDLINE=88142842; PubMed=2830497;
 RA Benesh P., Vigneron M., Perez D., Revel M., Chebath J.;
 RT "Interferon-responsive regulatory elements in the promoter of the
 RT human 2'-5'-oligo(A) synthetase gene.";
 RL Mol. Cell. Biol. 7:4498-4504(1987).
 RN [11]
 RN SEQUENCE OF 1-27 FROM N.A.
 RP TISSUE=Liver;
 RX MEDLINE=88283644; PubMed=2456211;
 RA Rutherford M.N., Hannigan G.E., Williams B.R.G.;
 RT "Interferon-induced binding of nuclear factors to promoter elements
 RT of the 2-5A synthetase gene.";
 RL EMBO J. 7:751-759(1988).
 RN [12]
 RN MUTAGENESIS OF CVS-331; PHE-332 AND LYS-333.
 RX MEDLINE=98070528; PubMed=9407111;
 RA Ghosh A., Sarkar S.N., Guo W., Bandyopadhyay S., Sen G.C.;
 RT "Enzymatic activity of 2'-5'-oligoadenylate synthetase is impaired by
 RT specific mutations that affect oligomerization of the protein.";
 RL J. Biol. Chem. 272:33220-33226(1997).
 RN [13]
 RN MUTAGENESIS OF ASP-75 AND ASP-77.
 RX MEDLINE=99395121; PubMed=10464285;
 RA Sarkar S.N., Ghosh A., Wang H.W., Sung S.S., Sen G.C.;
 RT "The nature of the catalytic domain of 2'-5'-oligoadenylate
 RT synthetases.";
 RL J. Biol. Chem. 274:25535-25542(1999).
 CC -!- FUNCTION: MAY PLAY A ROLE IN MEDIATING RESISTANCE TO VIRUS
 CC INFECTION, CONTROL OF CELL GROWTH, DIFFERENTIATION, AND APOPTOSIS.
 CC -!- CATALYTIC ACTIVITY: Binds double-stranded RNA and polymerizes ATP
 CC into ppp(A2'p5'A)n oligomers, which activate the latent RNase L
 CC that, when activated, cleaves single-stranded RNAs.
 CC -!- SUBUNIT: Homotrimer.
 CC -!- SUBCELLULAR LOCATION: ASSOCIATED WITH DIFFERENT SUBCELLULAR
 CC FRACTIONS SUCH AS MITOCHONDRIAL, NUCLEAR, AND ROUGH/SMOOTH
 CC MICROSOMAL FRACTIONS.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=p46; Synonyms=46 kDa, E18;
 CC IsoId=P00973-1; Sequence=Displayed;
 CC Name=p41; Synonyms=41 kDa, E16, 3-9;
 CC IsoId=P00973-2; Sequence=VSP_003738, VSP_003739;
 CC Name=p48; Synonyms=9-2;
 CC IsoId=P00973-3; Sequence=VSP_003740;
 CC -!- INDUCTION: By interferons.
 CC -!- SIMILARITY: Belongs to the 2-5A synthetase family.
 CC -!- CAUTION: Ref.8 sequence differs from that shown due to a
 CC frameshift in position 400.
 CC -!- CAUTION: Ref.4 sequence was originally thought to originate from

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2004, 08:50:22 ; Search time 13.7349 Seconds
(without alignments)
665.325 Million cell updates/sec

Title: US-09-996-617-2_COPY_1335_1429
Perfect score: 490
Sequence: 1 LHFVDQYREQLIARVTSVEV.....HLIMELWEGSKKGLPLSS 95

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	490	100.0	1192	T17255	hypothetical prote
2	75	15.3	482	AB2515	hypothetical prote
3	73.5	15.0	584	D81265	hypothetical prote
4	73.5	15.0	1260	GNJSL1	retrovirus-related
5	73	14.9	363	SYM502	(2'-5')oligo(A) sy
6	71	14.5	137	C71005	hypothetical prote
7	71	14.5	833	H95029	leucyl-tRNA synthet
8	70	14.3	132	S15661	(2'-5')oligo(A) sy
9	70	14.3	691	D90592	hypothetical prote
10	70	14.3	1269	F84730	probable myosin he
11	69.5	14.2	384	SYHU16	(2'-5')oligo(A) sy
12	69.5	14.2	400	SYHU18	(2'-5')oligo(A) sy
13	69.5	14.2	414	SYM503	(2'-5')oligo(A) sy
14	69.5	14.2	459	A22842	(2'-5')oligo(A) sy
15	69.5	14.2	609	A43906	nuclear phosphopro
16	69	14.1	833	C97501	leucine-tRNA ligas
17	69	14.1	871	C72238	preprotein translo
18	68	13.9	1034	T30574	beta-galactosidase
19	67.5	13.8	192	F70487	conserved hypothet
20	67.5	13.8	204	MNN235	nonstructural prot
21	67.5	13.8	204	MNN283	nonstructural prot
22	67.5	13.8	344	B70136	flagellar motor sw
23	67.5	13.8	527	A82431	sensor protein Uhp
24	66.5	13.6	468	S21172	glutamate-tRNA lig
25	66	13.5	412	C88923	protein W03F9.1 [i
26	66	13.5	541	T48836	hypothetical prote
27	66	13.5	706	D82160	hypothetical prote
28	66	13.5	768	T27855	hypothetical prote
29	66	13.5	804	B89961	leucyl-tRNA synthet

30	65.5	13.4	279	2	C86774	transposase of IS9
31	65.5	13.4	279	2	C86836	transposase of IS9
32	65.5	13.4	279	2	H86780	transposase of IS9
33	65.5	13.4	322	2	A69963	hypothetical prote
34	65.5	13.4	374	2	G83711	hypothetical prote
35	65.5	13.4	374	2	T07033	transcription fact
36	65.5	13.4	954	2	H71427	hypothetical prote
37	65.5	13.4	1039	2	S18199	myosin heavy chain
38	65	13.3	308	2	D85879	hypothetical prote
39	65	13.3	39	2	E91035	hypothetical prote
40	65	13.3	358	2	S31407	(2'-5')oligo(A) sy
41	65	13.3	791	2	C95335	hypothetical prote
42	64.5	13.2	190	2	S23712	interferon alpha-I
43	64.5	13.2	430	2	A40559	long-chain-acyl-Co
44	64.5	13.2	439	2	D86440	unknown protein [i
45	64.5	13.2	524	2	D82285	GGDEF family prote

ALIGNMENTS

RESULT 1

TI7255
hypothetical protein DKFZp586O1822.1 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: TI7255
R.Kohrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A:Reference number: Z18722
A:Accession: TI7255
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1192 <KOE>
A:CROSS-references: EMBL:AL117470
A:Experimental source: adult uterus; clone DKFZp586O1822
C:Genetics:
A>Note: DKFZp586O1822.1

Query Match 100.0%; Score 490; DB 2; Length 1192;

Best Local Similarity 100.0%; Pred. No. 9.5e-41;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	LHFVDQYREQLIARVTSVEVLDKLHGQVLSQEQYRVLAENTRPSQMRKLFSLSQSWDR	60
DB	1098	LHFVDQYREQLIARVTSVEVLDKLHGQVLSQEQYRVLAENTRPSQMRKLFSLSQSWDR	1157

QY	61	KCKDGLYQALKETHPHLTMELWEGSKKGLPLSS	95
DB	1158	KCKDGLYQALKETHPHLTMELWEGSKKGLPLSS	1192

RESULT 2

AB2515
hypothetical protein alr7298 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120a
C:Species: Nostoc sp. PCC 7120
A>Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AB2515
R.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
Nakazaki, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, .
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AB2515
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-482 <KUE>
A:CROSS-references: GB:BA000020; PIDN:BAB78382.1; PID:q17135836; GSPDB:GN00180
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr7298
A:Genome: plasmid

H95029
leucyl-tRNA synthetase [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C:Accession: H95029
R:Tettelin, R.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
son, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a Virulent Isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: H95029
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-833 <KUR>
A:Cross-references: GB:AE005672; PIDN:AAK74433.1; PID:g14971724; GSPDB:GN00164; TIGR:SP4
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP0254
C:Superfamily: leucine-tRNA ligase

Query Match 14.5%; Score 71; DB 2; Length 833;
Best Local Similarity 25.3%; Pred. No. 42;
Matches 24; Conservative 21; Mismatches 38; Indels 12; Gaps 4;

QY 6 QYREQLIARTSVTVV-----LDKLHGQVLS--QYQYERVLAEATRPQMKRLFSLSQS 57
DB 659 KFLDRVRLITSKEILAEAGALDKVYNETVAVTBOIES-LKFNATIAQLMVFVNAANK 717

QY 58 WDRCKD---GLYQALKETHPHLMELWEKSGKKG 89
DB 718 EDKLYVDYAKGFQLIAPFAPHLABELWQTVABTG 752

RESULT 8
S15661
(2'-5')oligo(A) synthetase (EC 2.7.7.-) L1 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 16-Jul-1999
C:Accession: S15661; S19108
R:Rutherford, M.N.; Kumar, A.; Nissim, A.; Chebath, J.; Williams, B.R.G.
Nucleic Acids Res. 19, 1917-1924, 1991
A:Title: The murine 2-5A synthetase locus: three distinct transcripts from two linked ge
A:Reference number: S15660; MUID:91232962; PMID:1709495
A:Accession: S15661
A:Molecule type: mRNA
A:Residues: 1-192 <RUT>
A:Cross-references: EMBL:X55982
R:Williams, B.
submitted to the EMBL Data Library, September 1990
A:Reference number: S19108
A:Accession: S19108
A:Molecule type: mRNA
A:Residues: 1-175, 'L', 177-192 <WIL>
A:Cross-references: EMBL:X55982; NID:g49714; PIDN:CAA39455.1; PID:g49715
C:Superfamily: oligo(A) synthetase
C:Keywords: nucleotidyl transferase

Query Match 14.3%; Score 70; DB 2; Length 192;
Best Local Similarity 33.3%; Pred. No. 9.3;
Matches 17; Conservative 9; Mismatches 17; Indels 8; Gaps 2;

QY 42 NTRPSQMKRLFSLSQSDRKCKDGLYQALKETHPHLMEL-----WEKSGSK 87
DB 137 NCRPTKRLRLIRLTHWYQICKKGLGDLPL---PQVALELLTVDAMEYGSR 184

RESULT 9
D90592
hypothetical protein MYP01_6440 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 22-Jun-2003

C:Accession: D90592
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pul
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: D90592
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-691 <KUR>
A:Cross-references: GB:AL445565; PID:g14090059; PIDN:CAC13817.1; GSPDB:GN00153
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYP01_6440
C:Superfamily: pullulanase type debranching enzyme

Query Match 14.3%; Score 70; DB 2; Length 691;
Best Local Similarity 20.8%; Pred. No. 42;
Matches 25; Conservative 21; Mismatches 34; Indels 40; Gaps 4;

QY 1 LHFVDQYREQLIARTSVTVVLDKLHGQVLSQEQYERVL-----AENT 43
DB 274 IEFDRFIEE---AHKNGIAVIMDYVYVNMNMNMLNKDYFFRENSQILPVDDFAINT 330

QY 44 RPSQMKL-----FSLSQSDRKCKDGLYQALKETHPHLM--ELWE 83
DB 331 ESKMVRKLIIDSLVYFVEYFKVDGFRDLDLTFIDDKTLNLIFKLLKINPNIILHGEAWE 390

RESULT 10
F84730
Probable myosin heavy chain [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: F84730
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: F84730
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1269 <STO>
A:Cross-references: GB:AE002093; NID:g6598483; PIDN:AAC69932.2; GSPDB:GN00139
C:Genetics:
A:Gene: At2g32240
A:Map position: 2

Query Match 14.3%; Score 70; DB 2; Length 1269;
Best Local Similarity 29.2%; Pred. No. 87;
Matches 26; Conservative 22; Mismatches 33; Indels 8; Gaps 5;

QY 8 REQLIARTSVTVVLDKLHG--QVLSQEQYERVL-AENTRPSQMKRLFSLSQSDRKCKD 64
DB 120 KDELLSAKLEET-EKKHGDLEVVQKQKEVEERHSSQLKSLDALQSHDAKDE 178

QY 65 GLYQALKETHPHLMELWEKSGSKGLPL 93
DB 179 --LTVKAPFADALGIEL--ESSRKKLIEL 203

RESULT 11
SVHU16
(2'-5')oligo(A) synthetase (EC 2.7.7.-), splice form El6 - human
N:Alternate names: oligoadenylate synthetase
C:Species: Homo sapiens (man)
C>Date: 14-Nov-1983 #sequence_revision 28-Dec-1987 #text_change 21-Jul-2000
C:Accession: A91013; JS0012; A23623; A01204; A24359
R:Benech, P.; Mory, Y.; Revel, M.; Chebath, J.
EMBO J. 4, 2249-2256, 1985
A:Title: Structure of two forms of the interferon-induced (2'-5') oligo A synthetase of

A:Reference number: A91013; MUID:86081732; PMID:2416561
A:Accession: A91013
A:Molecule type: mRNA
A:Residues: 1-364 <BEN>
A:Cross-references: GB:X02874; GB:K00006; NID:g35122; PIDN:CAA26633.1; PID:g95123
R:Shojiiri, S.; Fukunaga, R.; Ichii, Y.; Sokawa, Y.
J. Biochem. 99, 1455-1464, 1986
A:Title: Structure and expression of a cloned cDNA for human (2'-5')oligoadenylate synthetase
A:Reference number: A32003; MUID:86223945; PMID:3754863
A:Accession: J50012
A:Molecule type: mRNA
A:Residues: 1-30, 'N', 32-114, 'F', 116-364 <SHI>
A:Cross-references: GB:D00068; GB:N00068; NID:g220080; PIDN:BAA00047.1; PID:g220081
R:Wathelet, M.; Moutschen, S.; Cravador, A.; Dewit, L.; Defilippi, P.; Huez, G.; Content
FEBS Lett. 196, 113-120, 1986
A:Title: Full-length sequence and expression of the 42 kDa 2-5A synthetase induced by hu
A:Reference number: A23623; MUID:86108911; PMID:3753689
A:Accession: A23623
A:Molecule type: mRNA
A:Residues: 1-30, 'N', 32-114, 'F', 116-294, 'T', 296-314, 'R', 316-364 <WAT>
A:Cross-references: GB:X04371; GB:M25352; NID:g23792; PIDN:CAB51602.1; PID:g5650578
C:Comment: This enzyme, one of those induced by interferons, binds double-stranded RNA a
C:Comment: For alternate splice forms, see PIR:SYHU18 and PIR:A22842.
C:Genetics:
A:Gene: GDB:OIAS
A:Cross-references: GDB:l19465; OMIM:164350
A:Map position: 12pter-12qter
C:Superfamily: oligo(A) synthetase
C:Keywords: alternative splicing; nucleotidyltransferase

Query Match 14.2%; Score 69.5; DB 1; Length 364;
Best Local Similarity 32.0%; Pred. No. 22; Mismatches 15; Indels 9; Gaps 2;
Matches 16; Conservative 10

QY 44 RPSQWRKLFSLSQSWDRKCKDGLYQALKETHPHILMEL-----WEKGSKK 88
DB 201 RPTKLKSLRLVKGHWYQNCCK---KLGKLPPOYALELLTVYAWERGSMMK 246

RESULT 12
SYHU18
(2'-5')oligo(A) synthetase (EC 2.7.7.-), splice form B18 - human
N:Alternate names: oligoadenylate synthetase
C:Species: Homo sapiens (man)
C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 20-Apr-2000
C:Accession: B24359; I57630, I37997
R:Benesh, P.; Moriy, Y.; Revel, M.; Chebath, J.
EMBO J. 4, 2249-2256, 1985
A:Title: Structure of two forms of the interferon-induced (2'-5') oligo A synthetase of
A:Reference number: A91013; MUID:86081732; PMID:2416561
A:Accession: B24359
A:Molecule type: mRNA
A:Residues: 1-400 <BEN>
A:Cross-references: GB:M1810; GB:K00006; GB:X02875; NID:g189322; PIDN:AB59553.1; PID:g
R:Benesh, P.; Vigneron, M.; Peretz, D.; Revel, M.; Chebath, J.
Mol. Cell. Biol. 7, 4498-4504, 1987
A:Title: Interferon-responsive regulatory elements in the promoter of the human 2',5'-ol
A:Reference number: I57630; MUID:88142842; PMID:2830497
A:Accession: I57630
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 2-28 <RES>
A:Cross-references: GB:M18099; NID:g189326; PIDN:AAA59955.1; PID:g553604
R:Wathelet, M.G.; Clausen, I.M.; Nols, C.B.; Content, J.; Huez, G.A.
Eur. J. Biochem. 169, 313-321, 1987
A:Title: New inducers revealed by the promoter sequence analysis of two interferon-activ
A:Reference number: I37997; MUID:88082760; PMID:3121313
A:Accession: I37997
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-28 <RES>
A:Cross-references: EMBL:X06560; NID:g34393; PIDN:CAA29803.1; PID:g34394

C:Comment: For alternate splice forms, see PIR:SYHU16 and PIR:A22842.
C:Genetics:
A:Gene: GDB:OIAS
A:Cross-references: GDB:l19465; OMIM:164350
A:Map position: 12pter-12qter
C:Superfamily: oligo(A) synthetase
C:Keywords: alternative splicing; nucleotidyltransferase

Query Match 14.2%; Score 69.5; DB 1; Length 414;
Best Local Similarity 32.0%; Pred. No. 26; Mismatches 15; Indels 9; Gaps 2;
Matches 16; Conservative 10

QY 44 RPSQWRKLFSLSQSWDRKCKDGLYQALKETHPHILMEL-----WEKGSKK 88
DB 201 RPTKLKSLRLVKGHWYQNCCK---KLGKLPPOYALELLTVYAWERGSMMK 246

RESULT 14
A22842
(2'-5')oligo(A) synthetase (EC 2.7.7.-), splice form 8-2 - human
C:Species: Homo sapiens (man)
C>Date: 20-Aug-1987 #sequence_revision 20-Apr-2000 #text_change 21-Jul-2000
C:Accession: A22842; A91013
R:Saunders, M.E.; Gewirt, D.R.; Tugwell, M.E.; McMahon, M.; Williams, B.R.G.
EMBO J. 4, 1761-1768, 1985
A:Title: Human 2-5A synthetase: characterization of a novel cDNA and corresponding gene
A:Reference number: A22842; MUID:85284966; PMID:2411547
A:Accession: A22842
A:Molecule type: mRNA
A:Residues: 231-459 <SAU>
A:Cross-references: GB:X02661; NID:g23795; PIDN:CAA26497.1; PID:g1335008
R:Benesh, P.; Moriy, Y.; Revel, M.; Chebath, J.
EMBO J. 4, 2249-2256, 1985
A:Title: Structure of two forms of the interferon-induced (2'-5') oligo A synthetase of
A:Reference number: A91013; MUID:86081732; PMID:2416561
A:Accession: A91013
A:Molecule type: mRNA
A:Residues: 1-346; 'VRPPASSLFPFAPLHEA' <BEN>
A:Cross-references: GB:X02874; NID:g35122; PIDN:CAA26633.1; PID:g95123
C:Comment: This enzyme, one of those induced by interferons, binds double-stranded RNA a
C:Comment: For alternate splice forms, see PIR:SYHU18 and PIR:SYHU16.

Search completed: July 28, 2004, 08:55:19
Job time : 15.7349 secs

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OM protein - protein search, using sw model

Run on: July 28, 2004, 08:51:17 ; Search time 16:5964 Seconds
(without alignments)
295.514 Million cell updates/sec

Title: US-09-996-617-2_COPY_1335_1429

Perfect score: 490
Sequence: 1 LHFVDQYREQLIARTVTSVEV.....HLIMELWEXSKKGLPLSS 95

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pcp.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pcp.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pcp.*
5: /cgn2_6/ptodata/2/iaa/PCtUS COMB.pcp.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	253	51.6	193	4	US-09-340-620A-61
2	236	48.2	195	4	US-09-340-620A-49
3	216	44.1	71	4	US-09-340-620A-58
4	209	42.7	70	4	US-09-340-620A-57
5	209	42.7	70	4	US-09-340-620A-66
6	111.5	22.8	109	4	US-09-340-620A-71
7	72	14.7	164	4	US-09-245-281-41
8	72	14.7	164	4	US-09-207-359B-41
9	72	14.7	164	4	US-09-340-620A-41
10	72	14.7	164	4	US-09-865-364-41
11	72	14.7	249	4	US-09-245-281-39
12	72	14.7	249	4	US-09-207-359B-39
13	72	14.7	249	4	US-09-340-620A-39
14	72	14.7	249	4	US-09-865-364-39
15	72	14.7	409	4	US-09-207-359B-46
16	72	14.7	409	4	US-09-865-364-46
17	72	14.7	953	4	US-09-099-041A-8
18	72	14.7	953	4	US-09-245-281-8
19	72	14.7	953	4	US-09-245-281-43
20	72	14.7	953	4	US-09-207-359B-8
21	72	14.7	953	4	US-09-207-359B-43
22	72	14.7	953	4	US-09-340-620A-8
23	72	14.7	953	4	US-09-340-620A-43
24	72	14.7	953	4	US-09-865-364-8
25	72	14.7	953	4	US-09-865-364-43
26	72	14.7	966	4	US-09-207-359B-47
27	72	14.7	966	4	US-09-865-364-47

28 71.5 14.6 400 2 US-08-436-771-11 Sequence 11, Appl
29 71.5 14.6 400 2 US-08-434-998-11 Sequence 11, Appl
30 71.5 14.6 400 2 US-08-487-797-11 Sequence 11, Appl
31 71.5 14.6 400 5 PCT-US95-02058-11 Sequence 11, Appl
32 71 14.5 100 4 US-09-099-041A-10 Sequence 10, Appl
33 71 14.5 100 4 US-09-245-281-10 Sequence 10, Appl
34 71 14.5 100 4 US-09-207-359B-10 Sequence 10, Appl
35 71 14.5 100 4 US-09-340-620A-10 Sequence 10, Appl
36 71 14.5 100 4 US-09-865-364-10 Sequence 10, Appl
37 69.5 14.2 365 3 US-08-840-146-19 Sequence 19, Appl
38 69.5 14.2 365 3 US-09-360-220-19 Sequence 19, Appl
39 69 14.1 833 2 US-08-844-086-2 Sequence 2, Appl
40 69 14.1 833 3 US-09-018-211-2 Sequence 2, Appl
41 67.5 13.8 341 4 US-09-489-039A-12069 Sequence 12069, A
42 67.5 13.8 839 4 US-08-973-005A-11 Sequence 11, Appl
43 66.5 13.6 839 4 US-09-758-282B-206 Sequence 206, App
44 66 13.5 804 1 US-08-785-428-2 Sequence 2, Appl
45 66 13.5 804 2 US-08-996-797-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-340-620A-61

; Sequence 61, Application US/09340620A

; Patent No. 6482933

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF

; FILE REFERENCE: 07334-124001

; CURRENT APPLICATION NUMBER: US/09/340,620A

; CURRENT FILING DATE: 1999-06-28

; PRIOR APPLICATION NUMBER: US 09/245,281

; PRIOR FILING DATE: 1999-02-05

; PRIOR APPLICATION NUMBER: US 09/207,359

; PRIOR FILING DATE: 1998-12-08

; PRIOR APPLICATION NUMBER: US 09/099,041

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: US 09/019,942

; PRIOR FILING DATE: 1998-02-06

; NUMBER OF SEQ ID NOS: 71

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 61

; LENGTH: 193

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-340-620A-61

Query Match 51.6%; Score 253; DB 4; Length 193;

Best Local Similarity 61.2%; Pred. No. 3.5e-23; Mismatches 20; Indels 0; Gaps 0;

Matches 49; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

QY 2 HFVDQYREQLIARTVTSVEVYLDKLGQVLSQEQYERVLAEITRPSQMRKLFSLQSQSWDRK 61

Db 111 HFVDQHQALIAIVTVVDGVLDAHGSLVLTGGYQAVRAETTSQDKMRKLFSPVPSWNL 170

QY 62 CKDGLYQALKETHPHLIMEL 81

Db 171 CKDSLQALKEIHPYLVMDL 190

RESULT 2

US-09-340-620A-49

; Sequence 49, Application US/09340620A

; Patent No. 6482933

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF

; FILE REFERENCE: 07334-124001

; CURRENT APPLICATION NUMBER: US/09/340,620A

; CURRENT FILING DATE: 1999-06-28

; PRIOR APPLICATION NUMBER: US 09/245,281


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US-09-340-620A-71
; Sequence 71, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Consensus sequence
; NAME/KEY: VARIANT
; LOCATION: (1)...(109)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-340-620A-71

Query Match      22.8%; Score 111.5; DB 4; Length 109;
Best Local Similarity 42.0%; Pred. No. 3.6e-06;
Matches 34; Conservative 15; Mismatches 25; Indels 7; Gaps 4;

QY 4 VDQVREQLIARVTS--VEVVLDKLHGQ-VLSQEQYERVLAENTRPSQMRKLFSLQS--WD 59
DB 11 IDQHXALLARVTEDPXDSILDALSRDLISEBDYEAVEATTXLSKVRKLLILVQSKGE 70

QY 60 RKCK---DGLYQALKETHPHL 77
DB 71 ETCKXFLKLLQALKDSAAYL 91

RESULT 7
US-09-245-281-41
; Sequence 41, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/09/245,281
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: US 09/207,359
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 09/099,041
; EARLIER FILING DATE: 1998-06-17
; EARLIER APPLICATION NUMBER: US 09/019,942
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-245-281-41

Query Match      14.7%; Score 72; DB 4; Length 164;
Best Local Similarity 29.7%; Pred. No. 0.42;
Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;

QY 8 REQLIARVTSVEVVLDK-LHGQVLSQEQYERVLAENTRPSQMRKLFSLQSQSWDRKCKD-- 64
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US-09-340-620A-71
; Sequence 71, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-340-620A-41

Query Match      14.7%; Score 72; DB 4; Length 164;
Best Local Similarity 29.7%; Pred. No. 0.42;
Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;

QY 8 REQLIARVTSVEVVLDK-LHGQVLSQEQYERVLAENTRPSQMRKLFSLQSQSWDRKCKD-- 64
DB 27 RELLVTHIRNTQCLVDNLLKNDYFSAEDAIVCACTQPDVKRKILDLVQSGKEVSEFF 86

QY 65 -GLYQALKETHPHLIMELWEKSGKGLPLS 94
DB 87 LYLQQLADAYVDLRLPWLLEIGFSPSLTQS 117

RESULT 8
US-09-207-359B-41
; Sequence 41, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/207,359B
; CURRENT FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-207-359B-41

Query Match      14.7%; Score 72; DB 4; Length 164;
Best Local Similarity 29.7%; Pred. No. 0.42;
Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;

QY 87 LYLQQLADAYVDLRLPWLLEIGFSPSLTQS 117
DB 65 -GLYQALKETHPHLIMELWEKSGKGLPLS 94

RESULT 9
US-09-340-620A-41
; Sequence 41, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340,620A
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-340-620A-41

Query Match      14.7%; Score 72; DB 4; Length 164;
Best Local Similarity 29.7%; Pred. No. 0.42;
Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;

QY 87 LYLQQLADAYVDLRLPWLLEIGFSPSLTQS 117
DB 65 -GLYQALKETHPHLIMELWEKSGKGLPLS 94
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QY 8 REQLIARTVTSVEVLDK-LHGQVLSQEQYERVLAEINTPQSRKLFSLQSQWDRKCKD-- 64
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Db 27 RELVTHIRNTQCLVDNLLKNDYFSAEDAIVCACTQDKVRKILDVQSKGEEVSEFF 86
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QY 65 -GLYQALKETHPHLIMELWEKSKKGLPLS 94
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Db 87 LYLQQLADAYVDLRPWLEIGFSPSLTQS 117
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RESULT 10
US-09-865-364-41
; Sequence 41, Application US/09865364
; Patent No. 6613521
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/865,364
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-865-364-41

Query Match 14.7%; Score 72; DB 4; Length 164;
Best Local Similarity 29.7%; Pred. No. 0.42;
Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;

QY 8 REQLIARTVTSVEVLDK-LHGQVLSQEQYERVLAEINTPQSRKLFSLQSQWDRKCKD-- 64
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Db 27 RELVTHIRNTQCLVDNLLKNDYFSAEDAIVCACTQDKVRKILDVQSKGEEVSEFF 86
|||: : : : :|||: : : : :|||: : : : :|||: : : : :|||: : : : :
QY 65 -GLYQALKETHPHLIMELWEKSKKGLPLS 94
|||: : : : :|||: : : : :|||: : : : :|||: : : : :|||: : : : :
Db 87 LYLQQLADAYVDLRPWLEIGFSPSLTQS 117
|||: : : : :|||: : : : :|||: : : : :|||: : : : :|||: : : : :

RESULT 11
US-09-245-281-39
; Sequence 39, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/09/245,281
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: US 09/207,359
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 09/099,041
; EARLIER FILING DATE: 1998-06-17
; EARLIER APPLICATION NUMBER: US 09/019,942
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-245-281-39

Query Match 14.7%; Score 72; DB 4; Length 164;
Best Local Similarity 29.7%; Pred. No. 0.42;
Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;

QY 8 REQLIARTVTSVEVLDK-LHGQVLSQEQYERVLAEINTPQSRKLFSLQSQWDRKCKD-- 64
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RESULT 12
US-09-207-359B-39
; Sequence 39, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/207,359B
; CURRENT FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-207-359B-39

Query Match 14.7%; Score 72; DB 4; Length 249;
Best Local Similarity 29.7%; Pred. No. 0.72;
Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;

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QY 65 -GLYQALKETHPHLIMELWEKSKKGLPLS 94
|||: : : : :|||: : : : :|||: : : : :|||: : : : :|||: : : : :
Db 87 LYLQQLADAYVDLRPWLEIGFSPSLTQS 117
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RESULT 13
US-09-340-620A-39
; Sequence 39, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340,620A
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
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Query Match 14.7%; Score 72; DB 4; Length 249;
Best Local Similarity 29.7%; Pred. No. 0.72;
Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;

QY 8 REQLIARTVTSVEVLDK-LHGQVLSQEQYERVLAEINTPQSRKLFSLQSQWDRKCKD-- 64
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Db 27 RELVTHIRNTQCLVDNLLKNDYFSAEDAIVCACTQDKVRKILDVQSKGEEVSEFF 86
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QY 65 -GLYQALKETHPHLIMELWEKSKKGLPLS 94
|||: : : : :|||: : : : :|||: : : : :|||: : : : :|||: : : : :
Db 87 LYLQQLADAYVDLRPWLEIGFSPSLTQS 117
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RESULT 12
US-09-207-359B-39
; Sequence 39, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/207,359B
; CURRENT FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-207-359B-39

Query Match 14.7%; Score 72; DB 4; Length 249;
Best Local Similarity 29.7%; Pred. No. 0.72;
Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;

QY 8 REQLIARTVTSVEVLDK-LHGQVLSQEQYERVLAEINTPQSRKLFSLQSQWDRKCKD-- 64
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Db 27 RELVTHIRNTQCLVDNLLKNDYFSAEDAIVCACTQDKVRKILDVQSKGEEVSEFF 86
|||: : : : :|||: : : : :|||: : : : :|||: : : : :|||: : : : :
QY 65 -GLYQALKETHPHLIMELWEKSKKGLPLS 94
|||: : : : :|||: : : : :|||: : : : :|||: : : : :|||: : : : :
Db 87 LYLQQLADAYVDLRPWLEIGFSPSLTQS 117
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RESULT 13
US-09-340-620A-39
; Sequence 39, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340,620A
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
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OM protein - protein search, using sw model

Run on: July 28, 2004, 08:54:53 ; Search time 46.3554 Seconds

(without alignments)
642.856 Million cell updates/sec

Title: US-09-996-617-2_COPY_1335_1429

Perfect score: 490

Sequence: 1 LHFVDQYRQLIARTVTSVEV.....HLIMELWEKSGKGLPLSS 95

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	490	100.0	1399	9	US-09-388-221-4
2	490	100.0	1429	9	US-09-996-617-2
3	490	100.0	1429	9	US-09-931-071-2
4	490	100.0	1429	12	US-10-029-347-3
5	490	100.0	1429	12	US-10-029-347-26
6	490	100.0	1429	14	US-10-028-392-11
7	490	100.0	1429	14	US-10-028-374-3
8	490	100.0	1429	14	US-10-028-374-15
9	490	100.0	1429	14	US-10-183-770-3
10	490	100.0	1429	14	US-10-183-770-15
11	490	100.0	1443	9	US-09-388-221-6
12	490	100.0	1473	9	US-09-388-221-2
13	490	100.0	1473	12	US-10-182-822A-8
14	427	87.1	88	9	US-09-841-739-15
15	427	87.1	88	14	US-10-449-315-15

Sequence 139, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 61, Appli
Sequence 2, Appli
Sequence 61, Appli
Sequence 2, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 7, Appli
Sequence 49, Appli
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Sequence 5, Appli
Sequence 4, Appli
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Sequence 55, Appli
Sequence 84, Appli
Sequence 5, Appli
Sequence 5421, App
Sequence 145, App
Sequence 15, Appli
Sequence 59, Appli
Sequence 58, Appli
Sequence 57, Appli
Sequence 66, Appli
Sequence 57, Appli
Sequence 66, Appli
Sequence 146, App
Sequence 5422, Ap

404 5 82.6 442 10 US-09-895-298-139
17 253 51.6 84 9 US-09-841-879B-7
18 253 51.6 84 16 US-10-756-097-7
19 253 51.6 193 9 US-09-728-721-61
20 253 51.6 193 9 US-09-841-879B-2
21 253 51.6 193 14 US-10-295-981-61
22 253 51.6 193 16 US-10-756-097-2
23 236 48.2 85 9 US-09-841-879B-8
24 236 48.2 85 16 US-10-756-097-8
25 236 48.2 90 9 US-09-931-071-7
26 236 48.2 195 9 US-09-728-721-49
27 236 48.2 195 9 US-09-996-617-8
28 236 48.2 195 9 US-09-841-879B-5
29 236 48.2 195 12 US-10-446-046-4
30 236 48.2 195 14 US-10-295-981-49
31 236 48.2 195 15 US-10-240-145-55
32 236 48.2 195 15 US-10-131-410-84
33 236 48.2 195 16 US-10-756-097-5
34 236 48.2 205 14 US-10-106-698-5421
35 224 45.7 65 10 US-09-895-298-145
36 218 44.5 85 9 US-09-841-879B-15
37 218 44.5 85 16 US-10-756-097-15
38 216 44.1 71 9 US-09-728-721-58
39 216 44.1 71 14 US-10-295-981-58
40 209 42.7 70 9 US-09-728-721-57
41 209 42.7 70 9 US-09-728-721-66
42 209 42.7 70 14 US-10-295-981-57
43 209 42.7 70 14 US-10-295-981-66
44 180.5 36.8 59 10 US-09-895-298-146
45 127.5 26.0 158 14 US-10-106-698-5422

ALIGNMENTS

RESULT 1
US-09-388-221-4
; Sequence 4, Application US/09388221A
; Publication No. US20020192643A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. US20020192643A1el Card Proteins Involved in Cell Death Regu
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388, 221A
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 4
; LENGTH: 1399
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-388-221-4

Query Match 100.0%; Score 490; DB 9; Length 1399;
Best Local Similarity 100.0%; Pred. No. 7.3e-46;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYRQLIARTVTSVEVLDKLHGQVLSQEQYERVLAEINTRPSQMRKLFSLSQSWDR 60
DB 1305 LHFVDQYRQLIARTVTSVEVLDKLHGQVLSQEQYERVLAEINTRPSQMRKLFSLSQSWDR 1364
QY 61 KKCDGLYQALKETHPHLIMELWEKSGKGLPLSS 95
DB 1365 KKCDGLYQALKETHPHLIMELWEKSGKGLPLSS 1399

RESULT 2
US-09-996-617-2
; Sequence 2, Application US/09996617
; Patent No. US20020128198A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

Query Match 100.0%; Score 490; DB 14; Length 1429;
 Best Local Similarity 100.0%; Pred. No. 7.5e-46;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYREQLIARVTSVEVLDKLGQVLSQEQYERVAENTRPSQMRKLFSLSQSWDR 60
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 DB 1335 LHFVDQYREQLIARVTSVEVLDKLGQVLSQEQYERVAENTRPSQMRKLFSLSQSWDR 1394
 |||||

QY 61 KCKDGLYQALKETHPHLIMELWEKSGKGLPLSS 95
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 DB 1395 KCKDGLYQALKETHPHLIMELWEKSGKGLPLSS 1429
 |||||

RESULT 11
 US-09-388-221-6
 ; Sequence 6, Application US/09388221A
 ; Publication No. US20020192643A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, John C.
 ; TITLE OF INVENTION: No. US20020192643A1e1 Card Proteins Involved in Cell Death Regul
 ; FILE REFERENCE: P-LJ 3650
 ; CURRENT APPLICATION NUMBER: US/09/388,221A
 ; CURRENT FILING DATE: 1999-09-01
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 1443
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-388-221-6

Query Match 100.0%; Score 490; DB 9; Length 1443;
 Best Local Similarity 100.0%; Pred. No. 7.6e-46;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1349 LHFVDQYREQLIARVTSVEVLDKLGQVLSQEQYERVAENTRPSQMRKLFSLSQSWDR 1408
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QY 61 KCKDGLYQALKETHPHLIMELWEKSGKGLPLSS 95
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 DB 1409 KCKDGLYQALKETHPHLIMELWEKSGKGLPLSS 1443
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RESULT 12
 US-09-388-221-2
 ; Sequence 2, Application US/09388221A
 ; Publication No. US20020192643A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, John C.
 ; TITLE OF INVENTION: No. US20020192643A1e1 Card Proteins Involved in Cell Death Regul
 ; FILE REFERENCE: P-LJ 3650
 ; CURRENT APPLICATION NUMBER: US/09/388,221A
 ; CURRENT FILING DATE: 1999-09-01
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 1473
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-388-221-2

Query Match 100.0%; Score 490; DB 9; Length 1473;
 Best Local Similarity 100.0%; Pred. No. 7.8e-46;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYREQLIARVTSVEVLDKLGQVLSQEQYERVAENTRPSQMRKLFSLSQSWDR 60
 |||||
 DB 1379 LHFVDQYREQLIARVTSVEVLDKLGQVLSQEQYERVAENTRPSQMRKLFSLSQSWDR 1438
 |||||

QY 61 KCKDGLYQALKETHPHLIMELWEKSGKGLPLSS 95
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DB 1439 KCKDGLYQALKETHPHLIMELWEKSGKGLPLSS 1473

RESULT 13
 US-10-182-822A-8
 ; Sequence 8, Application US/10182822A
 ; Publication No. US20030211493A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE GENOMICS, INC.; BAUGHN, Mariah R.
 ; APPLICANT: AU-YOUNG, Janice; YUE, Henry
 ; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
 ; FILE REFERENCE: PI-0032 USN
 ; CURRENT APPLICATION NUMBER: US/10/182,822A
 ; CURRENT FILING DATE: 2001-02-01
 ; PRIOR APPLICATION NUMBER: PCT/US 01/03455
 ; PRIOR FILING DATE: 2001-01-02
 ; PRIOR APPLICATION NUMBER: US 60/180,093
 ; PRIOR FILING DATE: 2000-02-02
 ; PRIOR APPLICATION NUMBER: US 60/182,045
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 8
 ; LENGTH: 1473
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No: 4250893CD1
 US-10-182-822A-8

Query Match 100.0%; Score 490; DB 12; Length 1473;
 Best Local Similarity 100.0%; Pred. No. 7.8e-46;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 |||||
 DB 1379 LHFVDQYREQLIARVTSVEVLDKLGQVLSQEQYERVAENTRPSQMRKLFSLSQSWDR 1438
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QY 61 KCKDGLYQALKETHPHLIMELWEKSGKGLPLSS 95
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 DB 1439 KCKDGLYQALKETHPHLIMELWEKSGKGLPLSS 1473
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RESULT 14
 US-09-841-739-15
 ; Sequence 15, Application US/09841739
 ; Patent No. US20020034784A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bertin, John
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
 ; FILE REFERENCE: 07334-329001
 ; CURRENT APPLICATION NUMBER: US/09/841,739
 ; CURRENT FILING DATE: 2001-08-29
 ; PRIOR APPLICATION NUMBER: US 09/697,089
 ; PRIOR FILING DATE: 2000-10-26
 ; PRIOR APPLICATION NUMBER: US 60/161,822
 ; PRIOR FILING DATE: 1999-10-27
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 15
 ; LENGTH: 88
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-841-739-15

Query Match 87.1%; Score 427; DB 9; Length 88;
 Best Local Similarity 100.0%; Pred. No. 2.8e-40;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYREQLIARVTSVEVLDKLGQVLSQEQYERVAENTRPSQMRKLFSLSQSWDR 60
 |||||
 DB 7 LHFVDQYREQLIARVTSVEVLDKLGQVLSQEQYERVAENTRPSQMRKLFSLSQSWDR 66
 |||||

QY 61 KCKDGLYQALKETHPHLIMELW 82
Db 67 KCKDGLYQALKETHPHLIMELW 88

RESULT 15
US-10-449-315-15
; Sequence 15, Application US/10449315
; Publication No. US20030190679A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001 US/10/449,315
; CURRENT APPLICATION NUMBER: US/10/449,315
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US /09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-315-15

Query Match 87.1%; Score 427; DB 14; Length 88;
Best Local Similarity 100.0%; Pred. No. 2.8e-40;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYREQLIARVTSVEVVDKLGQVLSQFQYEVLAENTRPSQMEKLPSSLQSWDR 60
Db 7 LHFVDQYREQLIARVTSVEVVDKLGQVLSQFQYEVLAENTRPSQMEKLPSSLQSWDR 66

QY 61 KCKDGLYQALKETHPHLIMELW 82
Db 67 KCKDGLYQALKETHPHLIMELW 88

Search completed: July 28, 2004, 09:04:14
Job time : 47.3554 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2004, 08:46:11 ; Search time 54.9398 Seconds
(without alignments)
488.572 Million cell updates/sec

Title: US-09-996-617-2_COPY_1335_1429
Perfect score: 490
Sequence: 1 LHFVDQYRQLIARVTSVEV.....HLIMELWKGKGLPLSS 95

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	490	100.0	1397	4 AAY72670	Aay72670 Human NB-
2	490	100.0	1429	4 AAB62571	Aab62571 Human CAR
3	490	100.0	1429	5 ABG78455	Abg78455 Human cas
4	490	100.0	1429	5 ABG78472	Abg78472 Leucine-r
5	490	100.0	1429	5 ABB77916	Abb77916 Human leu
6	490	100.0	1429	5 ABG7969	Abg7969 Human leu
7	490	100.0	1429	5 AAO17855	Aao17855 Pyrin dom
8	490	100.0	1429	6 ABG71631	Abg71631 Human cas
9	490	100.0	1429	6 ABP96889	Abp96889 Human cas
10	490	100.0	1429	6 ABP96888	Abp96888 Human NAC
11	490	100.0	1429	6 ABG71633	Abg71633 Human cas
12	490	100.0	1442	4 AAY72671	Aay72671 Human NB-
13	490	100.0	1473	4 AAE06758	Aae06758 Human G-p
14	490	100.0	1473	4 AAY72669	Aay72669 Human NB-
15	490	100.0	1473	4 AAY72711	Aay72711 Human NAC
16	404.5	82.6	442	3 AAB24513	Aab24513 Human sec
17	253	51.6	193	4 AAB20086	Aab20086 Mouse CAR
18	253	51.6	193	4 AAE00592	Aae00592 Mouse tar
19	253	51.6	193	5 AAU93352	Aau93352 Mouse cas
20	236	48.2	84	4 AAE00591	Aae00591 Human tar
21	236	48.2	176	4 AAE00594	Aae00594 Alternati
22	236	48.2	195	2 AAY48553	Aay48553 Human bre
23	236	48.2	195	4 AAU68525	Aau68525 Human nov
24	236	48.2	195	4 AAB20085	Aab20085 Human CAR
25	236	48.2	195	4 AAE00588	Aae00588 Human tar

26	236	48.2	195	5 AAU99353	Aau99353 Human cas
27	236	48.2	195	5 AAO17854	Aao17854 Pyrin dom
28	236	48.2	195	6 ABG71635	Abg71635 Human cas
29	236	48.2	205	4 AAG74647	Aag74647 Human col
30	224	45.7	65	3 AAB24519	Aab24519 Human sec
31	216	44.1	171	4 AAE00593	Aae00593 Rat targe
32	180.5	36.8	59	3 AAB24520	Aab24520 Human sec
33	127.5	26.0	158	4 AAG74648	Aag74648 Human col
34	127.5	26.0	190	3 AAB43675	Aab43675 Human can
35	94.5	19.3	87	6 ABB82737	Abb82737 Human TUC
36	94.5	19.3	230	4 AAU21812	Aau21812 Novel hum
37	94.5	19.3	230	7 ADC46453	Adc46453 Human neo
38	94.5	19.3	431	4 AAB62572	Aab62572 Human CAR
39	94.5	19.3	431	4 AAY72672	Aay72672 Human CAR
40	94.5	19.3	431	6 ABU03496	Abu03496 Angiogene
41	94.5	19.3	431	6 ABG71632	Abg71632 Human cas
42	94.5	19.3	431	6 ABB82736	Abb82736 Human TUC
43	94.5	19.3	431	6 ABG71634	Abg71634 Human cas
44	94.5	19.3	488	4 AAU21689	Aau21689 Novel hum
45	94.5	19.3	488	7 ADC46330	Adc46330 Human neo

ALIGNMENTS

RESULT 1

AAV72670

ID AAY72670 standard; protein; 1397 AA.

XX

AC AAY72670;

XX

DT 31-MAY-2001 (first entry)

XX

DE Human NB-ARC and CARD containing protein (NAC) gamma isoform.

XX

KW Human; NB domain; nucleotide binding domain; NB-ARC and CARD; NAC;

KW caspase-associated recruitment domain; CARD; TIM-Barrel-like domain;

KW cysteine aspartyl protease; apoptosis; cytokine production;

KW cytokine receptor signalling; therapy; inflammatory disorder; sepsis;

KW fibrosis; arthritis; cancer; adenocarcinoma; leukaemia.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 1..956

FT /note= "Corresponds to 1-956 residues of human NAC beta

FT isoform (AAY72669)"

FT 957..1229

FT Region /note= "Corresponds to 988-1260 residues of human NAC

FT beta isoform (AAY72669)"

FT 1230..1397

FT Region /note= "Corresponds to 1306-1473 residues of human NAC

FT beta isoform (AAY72669)"

XX WO200116170-A2.

PN

XX AAO17855 Pyrin dom

PD 08-MAR-2001.

XX

PF 01-SEP-2000; 2000WO-US024152.

XX

PR 01-SEP-1999; 99US-00388221.

XX (BURN-) BUENHAM INST.

 PA | Reed JC; |

PS Claim 15; Page 143-148; 184pp; English.

XX The present sequence is a human NB-ARC and CARD containing protein (NAC)

CC gamma isoform. NAC gamma isoform represents the NAC splice variant in

CC which both the splice regions are absent in the translated polypeptide.

CC NAC protein comprises a nucleotide binding (NB) domain (also referred as

CC NB-ARC domain), a caspase-associated recruitment domain (CARD) and a TIM-

CC Barrel-like domain. The caspases, cysteine aspartyl proteases, are

CC principal effectors of apoptosis. CARD containing NAC proteins are used

CC for screening modulators that modulates apoptosis, cytokine production,

CC cytokine receptor signaling and other cellular processes. NAC can act as

CC an immunogen for the production of polyclonal and monoclonal antibodies.

CC It can also be used to diagnose and treat inflammatory disorders such as

CC sepsis, fibrosis and arthritis and cancer pathologies such as

CC adenocarcinomas and leukaemias

XX Sequence 1397 AA;

SQ

Query Match 100.0%; Score 490; DB 4; Length 1397;

Best Local Similarity 100.0%; Pred. No. 2.2e-48;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYREQLIARTSVSEVVDLKHGVLSQEQYERVLAEPTPSQMRKLFSLSQSWDR 60

Db |||||

QY 1303 LHFVDQYREQLIARTSVSEVVDLKHGVLSQEQYERVLAEPTPSQMRKLFSLSQSWDR 1362

Db |||||

QY 61 KCKDGLYQALKETHPHLIMELWEKSKKGLPLSS 95

Db 1363 KCKDGLYQALKETHPHLIMELWEKSKKGLPLSS 1397

RESULT 2

AAB62571

ID AAB62571 standard; protein; 1429 AA.

XX AC AAB62571;

XX

DT 23-JUL-2001 (first entry)

XX Human CARD-7 polypeptide.

DE

XX CARD-7; CARD-8; CARD-5; caspase recruitment domain; cancer; human;

XX autoimmune disorder; antiinflammatory; immunosuppressive; antiallergic;

XX antibacterial; antiviral, gene therapy.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FH 329..645

FT Domain /note= "nucleotide binding domain"

FT 333..341

FT Domain /note= "kinase 1A subdomain"

FT 404..413

FT Domain /note= "kinase 2 subdomain"

FT 454..463

FT Domain /note= "kinase 3a subdomain"

FT 615..622

FT Domain /note= "motif 2 domain"

FT 807..834

FT Domain /note= "leucine-rich domain"

FT 836..863

FT Domain /note= "leucine-rich domain"

FT 864..891

FT Domain /note= "leucine-rich domain"

FT 893..920

FT Domain /note= "leucine-rich domain"

FT 921..948

FT Domain /note= "leucine-rich domain"

FT 950..976

FT Domain /note= "leucine-rich domain"

XX WO200130813-A1.

XX

PD 03-MAY-2001.

XX 27-OCT-2000; 2000WO-US029796.

XX 27-OCT-1999; 99US-00428252.

XX (MILL-) MILLENNIUM PHARM INC.

XX Bertin J;

XX WPI; 2001-343340/36.

DR N-PSDB; AAF83651.

XX

PT Identifying a modulator of interaction between caspase recruitment domain

PT (CARD)-7 and CARD-5, for treating autoimmune disorders, comprises

PT measuring the binding of CARD-7 and CARD-5 in the presence of the

PT compound.

XX Disclosure; Fig 1A-D; 80pp; English.

XX The invention relates to identifying compounds, that modulate interaction

XX between caspase recruitment domain (CARD)-7 and CARD-5. The method

XX involves measuring the binding of CARD-7 and CARD-5 in the presence of

XX the compound (an increase in the binding of CARD-7 to CARD-5 in the

XX presence of the compound compared to the binding in the absence of the

XX compound indicates that the compound is a modulator of CARD-7-CARD-5

XX interaction). Modulators of CARD-7 and CARD-8 expression or activity can

XX be used to treat or diagnose disorders such as cancers, bacterial or

XX viral infections, autoimmune disorders (systemic lupus erythematosus,

XX immune-mediated glomerulonephritis or arthritis), inflammatory disorders,

XX organ-specific autoimmunity including multiple sclerosis, Hashimoto's

XX thyroiditis, or Grave's disease, psoriasis, graft rejection, allergies.

XX CARD-7 and CARD-8 are useful as modulating agents in regulating a variety

XX of cellular processes including cell growth and cell death. The present

XX sequence represents the human CARD-7, an intracellular protein

SQ Sequence 1429 AA;

Query Match 100.0%; Score 490; DB 4; Length 1429;

Best Local Similarity 100.0%; Pred. No. 2.2e-48;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYREQLIARTSVSEVVDLKHGVLSQEQYERVLAEPTPSQMRKLFSLSQSWDR 60

Db |||||

QY 1335 LHFVDQYREQLIARTSVSEVVDLKHGVLSQEQYERVLAEPTPSQMRKLFSLSQSWDR 1394

Db |||||

QY 61 KCKDGLYQALKETHPHLIMELWEKSKKGLPLSS 95

Db 1395 KCKDGLYQALKETHPHLIMELWEKSKKGLPLSS 1429

RESULT 3

ABG78455

ID ABG78455 standard; protein; 1429 AA.

XX AC ABG78455;

XX

DT 15-NOV-2002 (first entry)

XX Human caspase recruitment protein 7 protein.

DE

XX Human; human leucine-rich repeat small intestine I; HLRRSII; asthma;

XX proliferative disorder; gastrointestinal disorder; renal disorder;

XX neural disorder; reproductive disorder; calcium regulation; apoptosis;

XX immune system; anaemia; human immune deficiency virus; HIV; cancer;

XX blood coagulation disorder; autoimmune disorder; allergic reaction;

XX inflammatory condition; cardiovascular disorder; ischaemia;

XX neurological disorder; infectious disease; cytokine production;

XX expressed sequence tag; Est.

XX Homo sapiens.

XX WO2000261086-A2.

XX

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XX 08-AUG-2002.
XX
XX 20-DEC-2001; 2001WO-US049739.
XX
XX 22-DEC-2000; 2000US-0257774P.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Feder J, Ramanathan C, Mintier G;
XX
XX WPI; 2002-619252/66.
XX
XX New isolated nucleic acid molecules encoding HLRS11 polypeptides, or
XX their fragments and homologues, useful for preventing, treating and
XX ameliorating medical conditions, e.g. proliferative, gastrointestinal, or
XX renal disorders.
XX
XX Disclosure; Fig 2; 336pp; English.
XX
XX The invention relates to isolated nucleic acid molecules (I) encoding
XX human leucine-rich repeat small intestine I (HLRS11) polypeptides. The
XX nucleic acid molecules and polypeptides are useful for preventing,
XX treating and ameliorating medical conditions, such as proliferative,
XX gastrointestinal, renal, neural, or reproductive disorders; or disorders
XX related to aberrant calcium regulation or apoptosis modulation, either
XX directly or indirectly. They are also useful for treating, preventing
XX and/or diagnosing diseases, disorders and/or conditions of: immune system
XX by activating or inhibiting the proliferation, differentiation, or
XX mobilisation of immune cells; haematopoietic cells e.g. thrombocytopenia,
XX anaemia; immunologic deficiency syndromes, e.g. human immune deficiency
XX virus (HIV) infection, HTLV-BLV infection; blood coagulation disorders,
XX e.g. arterial thrombosis; autoimmune disorders, e.g. Addison's disease,
XX myasthenia gravis; asthma or allergic reactions; inflammatory conditions,
XX e.g. chronic prostatitis, sepsis; proliferative disorders, e.g. cancer;
XX cardiovascular disorders, e.g. arrhythmia, myocardial ischaemias,
XX aneurysms; neurological disorders, e.g. Alzheimer's disease, Huntington's
XX chorea; infectious diseases, e.g. measles, mumps, pneumonia, or viral
XX bacterial, and fungal infections. The HLRS11 polypeptides are useful for
XX modulating cytokine production, antigen presentation, or other processes
XX such as boosting immune responses. ABG78474-ABG78474 represent HLRS11
XX amino acid sequences and related amino acid sequences of the invention
XX
XX Sequence 1429 AA;
XX
XX Query Match 100.0%; Score 490; DB 5; Length 1429;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-48;
XX Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LHFVDQYREQLIARVTSVEVLDKLGQVLSQEQYERVLAEINTRPSQMRKLFSLSQSWDR 60
XX |
XX |
XX |
XX 1335 LHFVDQYREQLIARVTSVEVLDKLGQVLSQEQYERVLAEINTRPSQMRKLFSLSQSWDR 1394
XX
XX QY 61 KCKDGLYQALKETHPHLIMELWEKSKKGLPLSS 95
XX |
XX |
XX |
XX 1395 KCKDGLYQALKETHPHLIMELWEKSKKGLPLSS 1429
XX
XX RESULT 4
XX ABG78472
XX ID ABG78472 standard; protein; 1429 AA.
XX
XX AC ABG78472;
XX
XX DT 15-NOV-2002 (first entry)
XX
XX Leucine-rich repeat (LRR) domain containing protein #2.
XX
XX Human; human leucine-rich repeat small intestine I; HLRS11; asthma;
XX proliferative disorder; gastrointestinal disorder; renal disorder;
XX neural disorder; reproductive disorder; calcium regulation; apoptosis;
XX immune system; anaemia; human immune deficiency virus; HIV; cancer;
XX blood coagulation disorder; autoimmune disorder; allergic reaction;

```

```

KW inflammatory condition; cardiovascular disorder; ischaemia;
KW neurological disorder; infectious disease; cytokine production;
KW expressed sequence tag; EST.
XX
XX Unidentified.
XX
XX WO200261086-A2.
XX
XX 08-AUG-2002.
XX
XX 20-DEC-2001; 2001WO-US049739.
XX
XX 22-DEC-2000; 2000US-0257774P.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Feder J, Ramanathan C, Mintier G;
XX
XX WPI; 2002-619252/66.
XX
XX New isolated nucleic acid molecules encoding HLRS11 polypeptides, or
XX their fragments and homologues, useful for preventing, treating and
XX ameliorating medical conditions, e.g. proliferative, gastrointestinal, or
XX renal disorders.
XX
XX Disclosure; Page 229-233; 336pp; English.
XX
XX The invention relates to isolated nucleic acid molecules (I) encoding
XX human leucine-rich repeat small intestine I (HLRS11) polypeptides. The
XX nucleic acid molecules and polypeptides are useful for preventing,
XX treating and ameliorating medical conditions, such as proliferative,
XX gastrointestinal, renal, neural, or reproductive disorders; or disorders
XX related to aberrant calcium regulation or apoptosis modulation, either
XX directly or indirectly. They are also useful for treating, preventing
XX and/or diagnosing diseases, disorders and/or conditions of: immune system
XX by activating or inhibiting the proliferation, differentiation, or
XX mobilisation of immune cells; haematopoietic cells e.g. thrombocytopenia,
XX anaemia; immunologic deficiency syndromes, e.g. human immune deficiency
XX virus (HIV) infection, HTLV-BLV infection; blood coagulation disorders,
XX e.g. arterial thrombosis; autoimmune disorders, e.g. Addison's disease,
XX myasthenia gravis; asthma or allergic reactions; inflammatory conditions,
XX e.g. chronic prostatitis, sepsis; proliferative disorders, e.g. cancer;
XX cardiovascular disorders, e.g. arrhythmia, myocardial ischaemias,
XX aneurysms; neurological disorders, e.g. Alzheimer's disease, Huntington's
XX chorea; infectious diseases, e.g. measles, mumps, pneumonia, or viral
XX bacterial, and fungal infections. The HLRS11 polypeptides are useful for
XX modulating cytokine production, antigen presentation, or other processes
XX such as boosting immune responses. ABG78454-ABG78474 represent HLRS11
XX amino acid sequences and related amino acid sequences of the invention
XX
XX Sequence 1429 AA;
XX
XX Query Match 100.0%; Score 490; DB 5; Length 1429;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-48;
XX Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LHFVDQYREQLIARVTSVEVLDKLGQVLSQEQYERVLAEINTRPSQMRKLFSLSQSWDR 60
XX |
XX |
XX |
XX 1335 LHFVDQYREQLIARVTSVEVLDKLGQVLSQEQYERVLAEINTRPSQMRKLFSLSQSWDR 1394
XX
XX Db 61 KCKDGLYQALKETHPHLIMELWEKSKKGLPLSS 95
XX |
XX |
XX |
XX 1395 KCKDGLYQALKETHPHLIMELWEKSKKGLPLSS 1429
XX
XX RESULT 5
XX ABG77916
XX ID ABG77916 standard; protein; 1429 AA.
XX
XX AC ABG77916;
XX
XX DT 07-OCT-2002 (first entry)
XX
XX

```

DE XX Human leucine-rich repeat domain containing protein KIAA0926.
 KW Human; leucine-rich repeat; HLRRBM1; proliferative disorder;
 KW immune condition; apoptosis; signal transduction; autoimmune disease;
 KW haematopoietic cell disease; graft-versus-host disease; allergy; asthma;
 KW cardiovascular disorder; neurological disease; pheromone;
 KW pulmonary disease; chronic obstructive pulmonary disease;
 KW allergic rhinitis; bronchial hyperresponsiveness; reproductive disease;
 KW haematopoietic disease; platelet disorder; Bernard-Soulier syndrome;
 KW inflammatory disorder; systemic lupus erythematosus;
 KW cardiovascular disease; cancer; KIAA0926.
 XX Homo sapiens.
 OS WO200252011-A2.
 PN 04-JUL-2002.
 PD 20-DEC-2001; 2001WO-US049740.
 PF 22-DEC-2000; 2000US-0257773P.
 PR (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA Feder J, Ramanathan C, Mintier G;
 XX WPI; 2002-566676/60.
 DR New HLRRBM1 nucleic acids for preventing, treating or ameliorating e.g.
 PT proliferative disorders, immune conditions, a disorder related to
 PT aberrant apoptosis modulation or developmental disorders.
 XX Example 1; Page 362-366; 371pp; English.
 PS The present sequence represents a human leucine-rich repeat domain
 CC containing protein, which was used as a probe to search for leucine-rich
 CC repeat containing protein HLRRBM1. HLRRBM1 polypeptides and
 CC polynucleotides are useful for preventing, treating or ameliorating a
 CC medical condition such as a proliferative disorder, immune condition, or
 CC a disorder related to aberrant apoptosis modulation, either directly or
 CC indirectly, and in modulating signal transduction activity in various
 CC cells, tissue and organisms. They are also useful for treating,
 CC preventing, or diagnosing diseases of haematopoietic cells, autoimmune
 CC disease, graft-versus-host disease, allergic conditions (e.g. asthma),
 CC cardiovascular disorders, and neurological diseases, and for increasing
 CC the organisms' ability to synthesize and/or release pheromones. The
 CC polypeptide may also be used in treating, preventing or ameliorating
 CC pulmonary disease (e.g. chronic obstructive pulmonary disease, allergic
 CC rhinitis, or bronchial hyperresponsiveness), reproductive disease,
 CC haematopoietic disease, platelet disorders (e.g. Bernard-Soulier
 CC syndrome), non-infectious disorders (e.g. innate immunity to bacterial
 CC pathogens, or adaptive immune response), immune and inflammatory
 CC disorders (e.g. systemic lupus erythematosus), cardiovascular diseases
 CC and cancers. HLRRBM1 nucleic acids may further be used in chromosome
 CC identification or mapping, as a chromosome marker, as molecular weight
 CC markers, as diagnostic probes, in gene therapy, in raising anti-DNA
 CC antibodies, or as antigens for eliciting immune responses
 XX Sequence 1429 AA;
 SQ Query Match 100.0%; Score 490; DB 5; Length 1429;
 Best Local Similarity 100.0%; Pred. No. 2.2e-48;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYREQLIARVTSVEVVDKLGQVLSQEQYERVLAEATRPQMRKLSLSQSWDR 60
 DB 1335 LHFVDQYREQLIARVTSVEVVDKLGQVLSQEQYERVLAEATRPQMRKLSLSQSWDR 1394
 QY 61 KCKDGLYQALKETHPHLIMELWEKSKGKLLPLSS 95
 DB 1395 KCKDGLYQALKETHPHLIMELWEKSKGKLLPLSS 1429

RESULT 6
 ABG97969
 ID ABG97969 standard; protein; 1429 AA.
 XX AC ABG97969;
 DT 07-JAN-2003 (first entry)
 XX DE Human leucine rich repeat domain containing protein #2.
 XX KW Leucine rich repeat; nervous system; human; neural disorder; apoptosis;
 KW renal disorder; immune disorder; arthritis; asthma; AIDS;
 KW acquired immunodeficiency syndrome; rheumatoid arthritis;
 KW haematopoietic disorder; metabolic disorder; reproductive disorder;
 KW pulmonary disease; cardiovascular disease; hyperproliferative disorder;
 KW neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
 KW Huntington's disease; developmental disorder; autoimmune disease;
 KW Addison's disease; haemolytic anaemia; antiphospholipid syndrome;
 KW allergic encephalomyelitis; gene therapy.
 XX OS Homo sapiens.
 XX PN WO200274959-A2.
 XX PD 26-SEP-2002.
 XX PF 20-DEC-2001; 2001WO-US050457.
 XX PR 03-JAN-2001; 2001US-0259479P.
 XX PR 09-JAN-2001; 2001US-0260616P.
 XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX PI Ramanathan C, Feder J, Mintier G;
 XX WPI; 2002-750554/81.
 XX PT New HLRRNS1 nucleic acids and polypeptides, useful for preventing,
 PT treating, or ameliorating e.g. renal disorder, immune, haematopoietic,
 PT metabolic, reproductive, pulmonary, cardiovascular or autoimmune
 PT diseases.
 XX Example 1; Page 392-397; 415pp; English.
 PS The invention describes nucleic acids encoding human leucine-rich repeat
 CC containing proteins expressed in nervous system tissues, HLRRNS1. The
 CC HLRRNS1 polypeptide or the polynucleotide is useful for preventing,
 CC treating, or ameliorating a neural disorder or a disorder related to
 CC aberrant apoptosis modulation (either directly or indirectly), renal
 CC disorder, immune disorder (e.g. arthritis, asthma, acquired
 CC immunodeficiency syndrome (AIDS) or rheumatoid arthritis),
 CC haematopoietic, metabolic, reproductive, pulmonary or cardiovascular
 CC diseases, hyperproliferative disorders, neurodegenerative diseases (e.g.
 CC Alzheimer's disease, Parkinson's disease or Huntington's disease),
 CC developmental disorders, non-infectious disorders, nervous system
 CC diseases and/or disorders, and autoimmune diseases (e.g. Addison's
 CC disease, haemolytic anaemia, antiphospholipid syndrome, or allergic
 CC encephalomyelitis). The polynucleotides are also useful as chromosome
 CC markers, for chromosome identification, gene therapy, and in identifying
 CC organisms from minute biological samples. This is the amino acid sequence
 CC of a leucine-rich repeat containing protein
 XX Sequence 1429 AA;
 SQ Query Match 100.0%; Score 490; DB 5; Length 1429;
 Best Local Similarity 100.0%; Pred. No. 2.2e-48;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYREQLIARVTSVEVVDKLGQVLSQEQYERVLAEATRPQMRKLSLSQSWDR 60
 DB 1335 LHFVDQYREQLIARVTSVEVVDKLGQVLSQEQYERVLAEATRPQMRKLSLSQSWDR 1394
 QY 61 KCKDGLYQALKETHPHLIMELWEKSKGKLLPLSS 95

[illegible]

CC etc). The present sequence represents human CARD-7

XX Sequence 1429 AA;

SQ

Query Match 100.0%; Score 490; DB 6; Length 1429;

Best Local Similarity 100.0%; Pred. No. 2.2e-48;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYRQLIARTVTSVEVLDKLGQVLSQEQYERVLAEVTRPSQVRKLFSLSQSWDR 60

Db 1335 LHFVDQYRQLIARTVTSVEVLDKLGQVLSQEQYERVLAEVTRPSQVRKLFSLSQSWDR 1394

QY 61 KCKDGLYQALKETHPHLMELWEKSKKGLPLSS 95

Db 1395 KCKDGLYQALKETHPHLMELWEKSKKGLPLSS 1429

RESULT 9

ABP96889
ID ABP96889 standard; protein; 1429 AA.

XX AC

ABP96889;

DT 16-JUN-2003 (first entry)

XX DE

Human caspase recruitment domain protein 7 SEQ ID NO:12.

XX KW

Human; cytostatic; neurotropic; neuroprotective; antiinflammatory;

XX KW antisense therapy; NAC; DEFCAP; hyperproliferative disease; apoptosis;

XX KW death effector filament-forming CED4-like apoptosis protein;

XX KW neurological disease; infection; inflammation; tumour formation;

XX KW caspase recruitment domain protein 7.

XX OS

Homo sapiens.

XX PN

WO2003024988-A1.

XX PD

27-MAR-2003.

PF 19-SEP-2002; 2002WO-US029664.

XX PR

19-SEP-2001; 2001US-00956712.

XX PA

(ISIS-) ISIS PHARM INC.

XX PI

Bennett CF, Freier SM;

XX DR

WPI; 2003-354583/33.

XX DR

N-PSDB; ACC45152.

XX PT New antisense compounds, useful for modulating the expression of NAC or

for treating a disease or condition associated with the expression of

PT NAC, e.g. hyperproliferative disease or neurological disease.

XX PS

Example 15; Page 121-128; 147pp; English.

XX The present invention describes a compound (I) 8-50 nucleobases in length

targeted to a nucleic acid molecule encoding NAC, where the compound

specifically hybridises with the nucleic acid molecule encoding NAC and

inhibits the expression of NAC. The compound specifically hybridises with

at least an 8-nucleobase portion of an active site on a nucleic acid

molecule encoding NAC. Also described: (1) a composition comprising (I)

and a pharmaceutical carrier or diluent; (2) inhibiting the expression of

(I); and (3) treating an animal having a disease or condition associated

with NAC comprising administering (I) to the animal so that expression of

NAC is inhibited. (I) has cytostatic, neurotropic, neuroprotective and

antiinflammatory activities, and can be used in antisense therapy. The

antisense compounds (I) are useful for modulating the expression of NAC,

and for treating a disease or condition associated with expression of

NAC, e.g. hyperproliferative disease, neurological disease, or a disease

or disorder arising from aberrant apoptosis. The compounds are also

useful as research reagents and kits, or for diagnostics, therapeutics

CC and prophylaxis, e.g. to prevent or delay infection, inflammation or

CC tumour formation. NAC is also known as a death effector filament-forming

CC CED4-like apoptosis protein (DEFCAP). NAC is located on human chromosome

CC 17p13. The present sequence represents a human caspase recruitment domain

CC protein 7, which is used in an example from the invention

XX SQ Sequence 1429 AA;

Query Match 100.0%; Score 490; DB 6; Length 1429;

Best Local Similarity 100.0%; Pred. No. 2.2e-48;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYRQLIARTVTSVEVLDKLGQVLSQEQYERVLAEVTRPSQVRKLFSLSQSWDR 60

Db 1335 LHFVDQYRQLIARTVTSVEVLDKLGQVLSQEQYERVLAEVTRPSQVRKLFSLSQSWDR 1394

QY 61 KCKDGLYQALKETHPHLMELWEKSKKGLPLSS 95

Db 1395 KCKDGLYQALKETHPHLMELWEKSKKGLPLSS 1429

RESULT 10

ABP96888

ID ABP96888 standard; protein; 1429 AA.

XX AC

ABP96888;

XX DT

16-JUN-2003 (first entry)

XX DE

Human NAC protein SEQ ID NO:3.

XX KW

Human; cytostatic; neurotropic; neuroprotective; antiinflammatory;

XX KW antisense therapy; NAC; DEFCAP; hyperproliferative disease; apoptosis;

XX KW death effector filament-forming CED4-like apoptosis protein;

XX KW neurological disease; infection; inflammation; tumour formation;

XX KW chromosome 17p13.

XX OS

Homo sapiens.

XX PN

WO2003024988-A1.

XX PD

27-MAR-2003.

XX PF

19-SEP-2002; 2002WO-US029664.

XX PR

19-SEP-2001; 2001US-00956712.

XX PA

(ISIS-) ISIS PHARM INC.

XX PI

Bennett CF, Freier SM;

XX DR

WPI; 2003-354583/33.

XX DR

N-PSDB; ACC45143.

XX PT New antisense compounds, useful for modulating the expression of NAC or

for treating a disease or condition associated with the expression of

PT NAC, e.g. hyperproliferative disease or neurological disease.

XX PS

Example 13; Page 81-88; 147pp; English.

XX The present invention describes a compound (I) 8-50 nucleobases in length

targeted to a nucleic acid molecule encoding NAC, where the compound

specifically hybridises with the nucleic acid molecule encoding NAC and

inhibits the expression of NAC. The compound specifically hybridises with

at least an 8-nucleobase portion of an active site on a nucleic acid

molecule encoding NAC. Also described: (1) a composition comprising (I)

and a pharmaceutical carrier or diluent; (2) inhibiting the expression of

NAC in cells or tissues comprising contacting the cells or tissues with

(I); and (3) treating an animal having a disease or condition associated

with NAC comprising administering (I) to the animal so that expression of

NAC is inhibited. (I) has cytostatic, neurotropic, neuroprotective and

antiinflammatory activities, and can be used in antisense therapy. The

antisense compounds (I) are useful for modulating the expression of NAC,

CC and for treating a disease or condition associated with expression of
CC NAC, e.g. hyperproliferative disease, neurological disease, or a disease
CC or disorder arising from aberrant apoptosis. The compounds are also
CC useful as research reagents and kits, or for diagnostics, therapeutics
CC and prophylaxis, e.g. to prevent or delay infection, inflammation or
CC tumour formation. NAC is also known as a death effector filament-forming
CC CSD4-like apoptosis protein (DEFCAP). NAC is located on human chromosome
CC 17p13. The present sequence represents human NAC, which is used in an
CC example from the present invention
XX
SQ Sequence 1429 AA;

Query Match 100.0%; Score 490; DB 6; Length 1429;
Best Local Similarity 100.0%; Pred. No. 2.2e-48;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYREQLIARVTSVEVLDKLGQVLSQYQYERVLAEINTPSQMRKLFSLSQSWDR 60
DB 1335 LHFVDQYREQLIARVTSVEVLDKLGQVLSQYQYERVLAEINTPSQMRKLFSLSQSWDR 1394
61 KCKDGLYQALKETHPHLMELWEKSGKGLPLSS 95
1395 KCKDGLYQALKETHPHLMELWEKSGKGLPLSS 1429

RESULT 11
ABG71633
ID ABG71633 standard; protein; 1429 AA.
XX
AC ABG71633;
DT 10-JAN-2003 (first entry)
DE Human caspase recruitment domain-7 (CARD-7).
XX
KW Human; caspase activity; caspase recruitment domain-7; CARD-7; caspase-1;
KW pseudo-interleukin-1 beta converting enzyme; IL-1beta; pseudoICE;
KW ICEBERG; cell growth; cell death; inflammation; apoptosis;
KW caspase activation; cancer; follicular lymphoma; leukaemia; melanoma;
KW colon cancer; lung carcinoma; viral infection; autoimmune disease;
KW systemic lupus erythematosus; reactive arthritis;
KW human immunodeficiency virus infection; HIV infection; ALS;
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW myocardial infarction; stroke; inflammatory disorder; Crohn's disease;
KW insulin dependent diabetes mellitus; multiple sclerosis; psoriasis;
KW graft rejection; allergic rhinitis; food allergy; conjunctivitis;
KW glomerular nephritis; cytostatic; virucide; immunosuppressive;
KW dermatological; nephrotropic; neuroprotective; cardiant.
XX
OS Homo sapiens.
XX
XX US2002128198-A1.
XX
PD 12-SEP-2002.
XX
XX 27-NOV-2001; 2001US-00996617.
XX
XX 28-JUN-1999; 99US-00340620.
XX
XX 27-OCT-1999; 99US-00428252.
XX
XX 15-AUG-2001; 2001US-00931071.
XX
XX (BERT)/ BERTIN J.
XX
XX Bertin J;
XX
XX WPI: 2003-028967/02.
XX
XX N-PSDB; ABS56030.
XX
XX Identifying modulator of CARD-7 and CARD-5 interaction, by contacting
XX CARD-7 and CARD-5 in presence of test compound, measuring their binding,
XX and identifying modulator, when binding of CARD-7 to CARD-5 is altered.
XX
XX Disclosure; Fig 1; 43pp; English.

XX The present invention relates to methods of identifying compounds that
CC regulate caspase activity using caspase recruitment domain-7 (CARD-7) or
CC caspase recruitment domain-8 (CARD-8). In particular, a method for
CC identifying a compound that modulates the interaction between CARD-8 and
CC caspase-1 pseudo-interleukin-1 (IL-1) beta converting enzyme (pseudoICE)
CC or ICEBERG is disclosed. CARD-7 and CARD-8 molecules are useful as
CC modulating agents in regulating a variety of cellular processes including
CC cell growth, cell death, and inflammation. The methods of the invention
CC are useful for identifying compounds that have the ability to
CC increase/decrease apoptosis, or comprise the ability to induce caspase
CC activation. The methods are useful for treating a disorder associated
CC with inappropriate apoptosis or inappropriate inflammation. The methods
CC are useful for treating disorders associated with an undesirably low rate
CC of apoptosis such as cancer (preferably follicular lymphoma, chronic
CC myelogenous leukaemia, melanoma, colon cancer, lung carcinoma, etc),
CC viral infections, autoimmune diseases caused by low levels of apoptosis
CC (e.g. systemic lupus erythematosus, immune-mediated glomerulonephritis,
CC and arthritis). The methods are also useful for treating disorders with
CC undesirably high rates of apoptosis such as human immunodeficiency virus
CC (HIV) infection, Alzheimer's disease, Parkinson's disease, amyotrophic
CC lateral sclerosis (ALS), retinitis pigmentosa, spinal muscular atrophy,
CC various forms of cerebellar degeneration, anaemia associated with chronic
CC disease, aplastic anaemia, chronic neutropenia, myelodysplastic
CC syndromes, myocardial infarction, stroke, and various inflammatory
CC disorders (e.g. Crohn's disease, reactive arthritis, insulin dependent
CC diabetes mellitus, multiple sclerosis, psoriasis, graft rejection,
CC allergic rhinitis, food allergies, conjunctivitis, glomerular nephritis,
CC etc). The present sequence represents human CARD-7
XX
SQ Sequence 1429 AA;

Query Match 100.0%; Score 490; DB 6; Length 1429;
Best Local Similarity 100.0%; Pred. No. 2.2e-48;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYREQLIARVTSVEVLDKLGQVLSQYQYERVLAEINTPSQMRKLFSLSQSWDR 60
DB 1335 LHFVDQYREQLIARVTSVEVLDKLGQVLSQYQYERVLAEINTPSQMRKLFSLSQSWDR 1394
61 KCKDGLYQALKETHPHLMELWEKSGKGLPLSS 95
1395 KCKDGLYQALKETHPHLMELWEKSGKGLPLSS 1429

RESULT 12
AAV72671
ID AAV72671 standard; protein; 1442 AA.
XX
AC AAV72671;
XX
XX 31-MAY-2001 (first entry)
XX
XX Human NB-ARC and CARD containing protein (NAC) delta isoform.
XX
XX Human; NB domain; nucleotide binding domain; NB-ARC and CARD; NAC;
XX caspase-associated recruitment domain; CARD; TM-Barrel-like domain;
XX cysteine aspartyl protease; apoptosis; cytokine production;
XX cytokine receptor signalling; therapy; inflammatory disorder; sepsis;
XX fibrosis; arthritis; cancer; adenocarcinoma; leukaemia.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Region 1..956
FT /note= "Corresponds to 1-956 residues of human NAC beta
FT isoform (AAV72669)"
FT 957..1442
FT Region
FT /note= "Corresponds to 988-1473 residues of human NAC
FT beta isoform (AAV72669)"
XX
XX WO200116170-A2.

PD 08-MAR-2001.
 XX
 PF
 XX 01-SEP-2000; 2000WO-US024152.
 XX
 PR 01-SEP-1999; 99US-00388221.
 XX
 PA (BURN-) BURNHAM INST.
 XX
 PI Reed JC;
 XX
 XX WPI; 2001-183258/18.
 DR N-PSDB; AAD02762.
 XX
 PT Novel nucleic acid encoding NB-ARC and caspase associated recruitment
 PT domains, used to produce polypeptides for screening for modulators of
 PT apoptosis.
 XX
 PS Claim 15; Page 154-158; 184pp; English.
 XX
 CC The present sequence is a human NB-ARC and CARD containing protein (NAC)
 CC delta isoform. NAC delta isoform represents the NAC splice variant in
 CC which one of the splice region is absent in the translated polypeptide.
 CC NAC protein comprises a nucleotide binding (NB) domain (also referred as
 CC NB-ARC domain), a caspase-associated recruitment domain (CARD) and a TIM-
 CC Barrel-like domain. The caspases, cysteine aspartyl proteases, are
 CC principal effectors of apoptosis. CARD containing NAC proteins are used
 CC for screening modulators that modulates apoptosis, cytokine production,
 CC cytokine receptor signalling and other cellular processes. NAC can act as
 CC an immunogen for the production of polyclonal and monoclonal antibodies.
 CC It can also be used to diagnose and treat inflammatory disorders such as
 CC sepsis, fibrosis and arthritis and cancer pathologies such as
 CC adenocarcinomas and leukaemias
 XX
 SQ Sequence 1442 AA;
 Query Match 100.0%; Score 490; DB 4; Length 1442;
 Best Local Similarity 100.0%; Pred. No. 2.2e-48; Indels 0; Gaps 0;
 Matches 95; Conservative 0; Mismatches 0
 QY 1 LHFVDQYREQIARTVSVEVLDKLGQVLSQEQYERVLAEINTPQSRKLFSLQSQWDR 60
 DB 1348 LHFVDQYREQIARTVSVEVLDKLGQVLSQEQYERVLAEINTPQSRKLFSLQSQWDR 1407
 QY 61 KCKDGLYQALKETHPHLIMELWEKSKKGLPLSS 95
 DB 1408 KCKDGLYQALKETHPHLIMELWEKSKKGLPLSS 1442
 RESULT 13
 AA06758
 ID AA06758 standard; protein, 1473 AA.
 XX
 AC AA06758;
 XX
 XX 16-OCT-2001 (first entry)
 XX
 DE Human G-protein coupled receptor-8 (GCREC-8) protein.
 XX
 KW Human; G-protein coupled receptor-8; GCREC-8; cytosolic; hepatotropic;
 KW virucide; antiinflammatory; anticonvulsant; antileptic; neuroprotective;
 KW nootropic; cerebroprotective; hypotensive; tranquiliser; vulnerary;
 KW ophthalmological; cell proliferative disorder; actinic keratosis;
 KW anorectic; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis;
 KW psoriasis; cancer; neurological disorder; stroke; Alzheimer's disease;
 KW Huntington's disease; Parkinson's disease; cardiovascular disorder;
 KW epilepsy; hypertension; varicose vein; vasculitis; dyspepsia;
 KW anorexia; gastrointestinal disorder; pancreatitis; autoimmune disorder;
 KW Addison's disease; Crohn's disease; acquired immune deficiency syndrome;
 KW AIDS; uveitis; infection; trauma; metabolic disorder; diabetes; obesity;
 KW osteoporosis; transgenic animal; gene therapy.
 OS Homo sapiens.
 XX

PH Key Location/Qualifiers
 FT Binding-site 334..341
 FT /label= ATP/GTP-binding_site
 FT /note= "P-loop"
 FT 1216..1237
 FT Domain
 FT /label= Transmembrane_domain
 XX
 PN WO200157085-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 01-FEB-2001; 2001WO-US003455.
 XX
 XX 02-FEB-2000; 2000US-0180093P.
 PR 11-FEB-2000; 2000US-0182045P.
 XX
 XX (INCY-) INCYTE GENOMICS INC.
 XX
 XX Baughn MR, Au-Young J, Yue H;
 PI WPI; 2001-488969/53.
 DR N-PSDB; AAD12951.
 XX
 PT Novel isolated human G-protein coupled receptor useful for diagnosing;
 PT preventing and treating cell proliferative, neurological, cardiovascular,
 PT gastrointestinal, autoimmune/inflammatory and metabolic disorders.
 XX
 PS Claim 1; Page 114-117; 138pp; English.
 XX
 CC The present sequence is human G-protein coupled receptor-8 (GCREC-8)
 CC encoding them. GCREC protein, its agonist or antagonist are useful for
 CC treating diseases or conditions associated with decreased expression or
 CC overexpression of functional GCREC in a patient, where the disorder is
 CC selected from cell proliferative disorders such as actinic keratosis,
 CC arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, psoriasis, and
 CC cancer, neurological disorders such as epilepsy, stroke, Alzheimer's
 CC disease, Huntington's disease, Parkinson's disease, cardiovascular
 CC disorders such as hypertension, vasculitis, varicose veins, gastro-
 CC intestinal disorders such as dysphagia, dyspepsia, anorexia, nausea,
 CC pancreatitis, autoimmune/inflammatory disorders such as acquired
 CC immunodeficiency syndrome (AIDS), Addison's disease, Crohn's disease,
 CC uveitis, viral, bacterial, fungal, parasitic, protozoal, helminthic
 CC infections, trauma and metabolic disorders such as diabetes, obesity,
 CC osteoporosis. GCREC proteins and their cDNAs are used to assess the
 CC effects of exogenous compounds on the expression of GCREC sequences.
 CC GCREC cDNA is useful to create knock in humanised animals (pigs) or
 CC transgenic animals (mice or rats) to model human disease, for therapeutic
 CC or diagnostic purposes, for somatic or germline gene therapy, to generate
 CC hybridisation probes useful in mapping the naturally occurring genomic
 CC sequence, and in molecular biological techniques
 XX
 SQ Sequence 1473 AA;
 Query Match 100.0%; Score 490; DB 4; Length 1473;
 Best Local Similarity 100.0%; Pred. No. 2.3e-48;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LHFVDQYREQIARTVSVEVLDKLGQVLSQEQYERVLAEINTPQSRKLFSLQSQWDR 60
 DB 1379 LHFVDQYREQIARTVSVEVLDKLGQVLSQEQYERVLAEINTPQSRKLFSLQSQWDR 1438
 QY 61 KCKDGLYQALKETHPHLIMELWEKSKKGLPLSS 95
 DB 1439 KCKDGLYQALKETHPHLIMELWEKSKKGLPLSS 1473
 RESULT 14
 AA072669
 ID AA072669 standard; protein, 1473 AA.
 XX
 AC AA072669;
 XX

DT 31-MAY-2001 (first entry)
 DE Human NB-ARC and CARD containing protein (NAC) beta isoform.
 XX Human; NB domain; nucleotide binding domain; NB-ARC and CARD; NAC;
 XX caspase-associated recruitment domain; CARD; TIM-Barrel-like domain;
 KW cysteine aspartyl protease; apoptosis; cytokine production;
 KW cytokine receptor signalling; therapy; inflammatory disorder; sepsis;
 KW fibrosis; arthritis; cancer; adenocarcinoma; leukaemia.
 XX Homo sapiens.
 OS
 PH Key Location/Qualifiers
 DE 329..547
 XX /label= NB domain
 FT /note= "Nucleotide binding domain, also designated as
 FT NB-ARC domain"
 FT 329..341
 FT /label= Walker_A
 FT /note= "Also designated as P-loop"
 FT 406..414
 FT /label= Walker_B
 FT 809..833
 FT /label= Leucine_rich_repeat_region
 FT 838..862
 FT /label= Leucine_rich_repeat_region
 FT 865..890
 FT /label= Leucine_rich_repeat_region
 FT 895..919
 FT /label= Leucine_rich_repeat_region
 FT 923..947
 FT /label= Leucine_rich_repeat_region
 FT 957..987
 FT /note= "This 31 amino acid segment is not found in NAC
 FT gamma isoform (AA72670) and NAC delta isoform (AA72671)
 FT due to alternative mRNA splicing"
 FT 1079..1364
 FT /note= "TIM-Barrel-like domain"
 FT 1128..1473
 FT /label= CARD-L
 FT /note= "Caspase-associated recruitment domain"
 FT 1128..1281
 FT /label= CARD-S
 FT /note= "Caspase-associated recruitment domain"
 FT 1261..1306
 FT /note= "This 45 amino acid segment is not found in NAC
 FT gamma isoform (AA72670) due to alternative mRNA
 FT splicing"
 FT 1306..1473
 FT /label= CARD-S
 FT /note= "Caspase-associated recruitment domain"
 FT 1373..1473
 FT /label= CARD
 FT /note= "Caspase-associated recruitment domain"
 FT
 XX WO200116170-A2.
 EN
 XX 08-MAR-2001.
 PD
 XX 01-SEP-2000; 2000WO-US024152.
 PF
 XX 01-SEP-1999; 99US-00388221.
 PR
 XX (BURN-) BURNHAM INST.
 PA
 XX Reed JC;
 XX
 XX WPI: 2001-183258/18.
 DR N-PSDB; AD02760.
 DR
 XX Novel nucleic acid encoding NB-ARC and caspase associated recruitment
 XX domains, used to produce polypeptides for screening for modulators of
 FT apoptosis.

XX Claim 15; Page 133-137; 184pp; English.
 PS
 XX The present sequence is a human NB-ARC and CARD containing protein (NAC)
 CC beta isoform. NAC beta isoform represents the NAC splice variant in which
 CC both the splice regions are present in the translated polypeptide. NAC
 CC protein comprises a nucleotide binding (NB) domain (also referred as NB-
 CC ARC domain), a caspase-associated recruitment domain (CARD) and a TIM-
 CC Barrel-like domain. The caspases, cysteine aspartyl proteases, are
 CC principal effectors of apoptosis. CARD containing NAC proteins are used
 CC for screening modulators that modulates apoptosis, cytokine production,
 CC cytokine receptor signalling and other cellular processes. NAC can act as
 CC an immunogen for the production of polyclonal and monoclonal antibodies.
 CC It can also be used to diagnose and treat inflammatory disorders such as
 CC sepsis, fibrosis and arthritis and cancer pathologies such as
 CC adenocarcinomas and leukaemias. Note: This sequence is stated as being
 CC the same as that shown as SEQ ID NO:2 (AA72711) in figure 1A of the
 CC specification. However the sequences differ at several positions
 XX
 SQ Sequence 1473 AA;
 Query Match 100.0%; Score 490; DB 4; Length 1473;
 Best Local Similarity 100.0%; Pred. No. 2.3e-48; Mismatches 0; Gaps 0;
 Matches 95; Conservative 0;
 QY 1 LHFVDQYREQLIARTVTSVEVLDKLHGQVLSQEQYERVLAEINTRPSQMKLFSLSQSWDR 60
 DB 1379 LHFVDQYREQLIARTVTSVEVLDKLHGQVLSQEQYERVLAEINTRPSQMKLFSLSQSWDR 1438
 QY 61 KCKDGLYQALKETHPHLINELWEKSKKGLPLSS 95
 DB 1439 KCKDGLYQALKETHPHLINELWEKSKKGLPLSS 1473
 RESULT 15
 AA72711
 ID AA72711 standard; protein; 1473 AA.
 XX
 AC AA72711;
 XX
 DT 31-MAY-2001 (first entry)
 XX
 DE Human NAC beta isoform, alternative version.
 XX
 KW Human; NB domain; nucleotide binding domain; NB-ARC and CARD; NAC;
 KW caspase-associated recruitment domain; CARD; TIM-Barrel-like domain;
 KW cysteine aspartyl protease; apoptosis; cytokine production;
 KW cytokine receptor signalling; therapy; inflammatory disorder; sepsis;
 KW fibrosis; arthritis; cancer; adenocarcinoma; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 DE 329..547
 XX /label= NB domain
 FT /note= "Nucleotide binding domain, also designated as
 FT NB-ARC domain"
 FT 329..341
 FT /label= Walker_A
 FT /note= "Also designated as P-loop"
 FT 406..414
 FT /label= Walker_B
 FT 809..833
 FT /label= Leucine_rich_repeat_region
 FT 838..862
 FT /label= Leucine_rich_repeat_region
 FT 865..890
 FT /label= Leucine_rich_repeat_region
 FT 895..919
 FT /label= Leucine_rich_repeat_region
 FT 923..947
 FT /label= Leucine_rich_repeat_region
 FT 957..987

```
FT /note= "This 31 amino acid segment is not found in NAC
FT gamma isoform (AAV72670) and NAC delta isoform (AAV72671)
FT due to alternative mRNA splicing"
FT 1079..1364
FT /note= "TIM-Barrel-like domain"
FT 1128..1473
FT /label= CARD-L
FT /note= "Caspase-associated recruitment domain"
FT 1128..1261
FT /label= CARD-S
FT /note= "Caspase-associated recruitment domain"
FT 1261..1306
FT /note= "This 45 amino acid segment is not found in NAC
FT gamma isoform (AAV72670) due to alternative mRNA
FT splicing"
FT 1298..1305
FT /note= "Encoded by GGGATGCTGGAAATACCTCCCAAG"
FT 1306..1473
FT /label= CARD-S
FT /note= "Caspase-associated recruitment domain"
FT 1373..1473
FT /label= CARD
FT /note= "Caspase-associated recruitment domain"
FT
XX WO200116170-A2.
XX PN
XX PD
XX PD
XX PD
XX 08-MAR-2001.
XX
XX 01-SEP-2000; 2000WO-US024152.
XX PF
XX
XX 01-SEP-1999; 99US-00398221.
XX PR
XX
XX (BURN-) BURNHAM INST.
XX PA
XX
XX Reed JC;
XX PI
XX
XX WPI; 2001-183258/18.
XX DR
XX N-PSDB; AAD02760.
XX
XX Novel nucleic acid encoding NB-ARC and caspase associated recruitment
XX domains, used to produce polypeptides for screening for modulators of
XX apoptosis.
XX
XX Claim 15; Fig 1A; 184pp; English.
XX
XX The present sequence is a human NB-ARC and CARD containing protein (NAC)
XX beta isoform, alternative version. NAC beta isoform represents the NAC
XX splice variant in which both the splice regions are present in the
XX translated polypeptide. NAC protein comprises a nucleotide binding (NB)
XX domain (also referred as NB-ARC domain), a caspase-associated recruitment
XX domain (CARD) and a TIM-Barrel-like domain. The caspases, cysteine
XX aspartyl proteases, are principal effectors of apoptosis. CARD containing
XX NAC proteins are used for screening modulators that modulates apoptosis,
XX cytokine production, cytokine receptor signalling and other cellular
XX processes. NAC can act as an immunogen for the production of polyclonal
XX and monoclonal antibodies. It can also be used to diagnose and treat
XX inflammatory disorders such as sepsis, fibrosis and arthritis and cancer
XX pathologies such as adenocarcinomas and leukaemias. Note: This sequence
XX is stated as being the same as that shown as SEQ ID NO:2 (See AAV72669)
XX in page 133-137 of the specification. However the sequences differ at
XX several positions
XX
XX Sequence 1473 AA;
XX
XX Query Match 100.0%; Score 490; DB 4; Length 1473;
XX Best Local Similarity 100.0%; Pred. No. 2.3e-48;
XX Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 LHFVDQYREQLIARTVSEVVLDKLGQVLSQEQYERVLAEENTRPSQMRKLFSLQSQWDR 60
XX
XX 1379 LHFVDQYREQLIARTVSEVVLDKLGQVLSQEQYERVLAEENTRPSQMRKLFSLQSQWDR 1438
XX
XX 61 KKDGLYQALKETHPHLIMELWEKSGKGLPLSS 95
```

Db

1439 KKDGLYQALKETHPHLIMELWEKSGKGLPLSS 1473

Search completed: July 28, 2004, 08:53:00
Job time : 56.9398 secs

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OM protein - protein search, using sw model

Run on: July 28, 2004, 08:46:11 ; Search time 41.0602 Seconds
(without alignments)
488.572 Million cell updates/sec

Title: US-09-996-617-8_COPY_111_181

Perfect score: 378
Sequence: 1 GLHFIDQHRALRIARTNVE.....LFSFTPAWNTCKDLLLQAL 71

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqp1980s:*
2: Geneseqp1980s:*
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4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	378	100.0	176	AAE00594	Alternati
2	378	100.0	195	AAV48553	Human bre
3	378	100.0	195	AAU68525	Human nov
4	378	100.0	195	AAE20085	Human CAR
5	378	100.0	195	AAE00588	Human tar
6	378	100.0	195	AAU99353	Human cas
7	378	100.0	195	AAO17854	Pyrim dom
8	378	100.0	195	ABG71635	Human cas
9	378	100.0	205	AAAG74647	Human col
10	372	98.4	84	AAE00591	Human tar
11	275	72.8	171	AAE00593	Rat targe
12	264	69.8	193	AAE20086	Mouse CAR
13	264	69.8	193	AAE00592	Mouse tar
14	264	69.8	193	AAU99352	Mouse tar
15	216	57.1	442	AAE24513	Human sec
16	216	57.1	1397	AAV72670	Human NB-
17	216	57.1	1429	AAE62571	Human CAR
18	216	57.1	1429	ABG78455	Human cas
19	216	57.1	1429	ABG78472	Human cas
20	216	57.1	1429	ABB77916	Leucine-r
21	216	57.1	1429	ABG77916	Human leu
22	216	57.1	1429	ABG97969	Human leu
23	216	57.1	1429	AAO17855	Human dom
24	216	57.1	1429	ABG71631	Human cas
25	216	57.1	1429	ABP96889	Human cas
26	216	57.1	1429	ABP96888	Human NAC

26	216	57.1	1429	6	ABG71633	Human cas
27	216	57.1	1442	4	AAV72671	Human NB-
28	216	57.1	1473	4	AAE06758	Human G-p
29	216	57.1	1473	4	AAV72669	Human NB-
30	216	57.1	1473	4	AAV72711	Human NAC
31	214	56.6	158	4	AAV74648	Human col
32	214	56.6	190	3	AAE43675	Human can
33	141	37.3	65	3	AAE24519	Human can
34	75	19.8	59	3	AAE24520	Human sec
35	69.5	18.4	93	5	ABJ04755	ARC prote
36	69.5	18.4	208	6	ABR58613	Human can
37	69.5	18.4	219	7	ADD48044	Human can
38	68.5	18.1	230	4	AAU21812	Human Pro
39	68.5	18.1	230	7	ADC46453	Human neo
40	68.5	18.1	431	4	AAE62572	Human CAR
41	68.5	18.1	431	4	AAV72672	Human CAR
42	68.5	18.1	431	6	ABU03496	Angiogene
43	68.5	18.1	431	6	ABG71632	Human cas
44	68.5	18.1	431	6	ABH82736	Human TUC
45	68.5	18.1	431	6	ABG71634	Human cas

ALIGNMENTS

RESULT 1
AAE00594
ID AAE00594 standard; protein; 176 AA.

AC AAE00594;

XX
XX
DT 02-JUL-2001 (first entry)

XX
DE Alternatively spliced form of human TMS1 protein (lacking exon2).

XX
KW Human; target of methylation-induced silencing-1; TMS1; cytostatic;
KW antiproliferative; apoptosis inducer; gene therapy; CpG island;
KW caspase-recruiting domain; CARD; cancer; breast.

XX
OS Homo sapiens.

XX
PN WO200129235-A2.

XX
PD 26-APR-2001.

XX
PF 18-OCT-2000; 2000WO-US028747.

XX
PR 18-OCT-1999; 99US-0159975P.

XX
PA (UYEM-) UNIV EMORY.

XX
PI Vertino PM;

XX
DR WPI; 2001-290922/30.

XX
DR N-PSDB; AAD03906.

XX
PT Novel gene TMS1, transcriptionally silenced due to increased methylation
PT useful for identifying subject at risk of developing tumor characterized
PT by abnormal methylation, for treating cancer by inducing apoptosis.

XX
PS Claim 85; Page 123; 124pp; English.

XX
CC The invention relates to identification of target of methylation-induced
CC silencing-1 (TMS1) gene. This gene is transcriptionally silenced due to
CC abnormal methylation of a CpG island in its 5' regulatory region. TMS1
CC consists of a carboxy terminal caspase-recruiting domain (CARD) and plays
CC a role in induction of apoptosis. TMS1 gene and protein are useful as
CC tools for diagnosing and treating a subject at risk of developing cancer
CC (e.g. breast cancer) characterized by abnormal CpG methylation or
CC abnormally low levels of TMS1 expression products. Unique fragments of
CC TMS1 gene are used as probes. TMS1 gene is useful in gene therapy. TMS1
CC molecule is also useful for treating abnormal cell proliferation by
CC increasing TMS1 polypeptide level to an above normal level. The Cpg

CC island region of TMS1 or its fragments are used to study the methylation
 CC patterns apart from any coding region contained in it. The present
 CC sequence is alternatively spliced form of human target of methylation-
 CC induced silencing-1 (TMS1) protein lacking exon2
 XX
 SQ Sequence 176 AA;
 Query Match 100.0%; Score 378; DB 4; Length 176;
 Best Local Similarity 100.0%; Pred. No. 3.2e-40;
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLHFIDQHRALIAIARVTVNVEWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSTPAWN 60
 DB 92 GLHFIDQHRALIAIARVTVNVEWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSTPAWN 151
 QY 61 WTCKDLLLQAL 71
 DB 152 WTCKDLLLQAL 162
 RESULT 2
 AAU68525
 ID AAU68525 standard; protein; 195 AA.
 AC AAU68525;
 DT 08-DEC-1999 (first entry)
 DE Human breast tumour-associated protein 14.
 KW Expressed sequence tag; EST; human; breast; cancer; gene therapy;
 KW treatment; tumour; cytostatic; medicament.
 XX Homo sapiens.
 OS
 PN DE19813839-A1.
 XX
 PD 23-SEP-1999.
 XX
 PF 20-MAR-1998; 98DE-01013839.
 XX
 PR 20-MAR-1998; 98DE-01013839.
 XX
 PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
 XX
 PI Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
 WPI; 1999-528981/45.
 DR N-PSDB; AAZ33631.
 XX
 PT Human nucleic acid sequences and protein products from tumor breast
 PT tissue, useful for breast cancer therapy.
 XX
 PS Claim 22; 149; 188pp; German.
 XX
 CC This invention describes novel human nucleic acid sequences from tumor
 CC breast tissue which have cytostatic activity. The nucleic acid sequences
 CC can be used to produce and isolate full-length gene sequences. They can
 CC be used to express proteins, which can be used as tools to find an
 CC activity against breast cancer. The sequences can be used in sense or
 CC antisense form. They are especially useful for medicaments for gene
 CC therapy to treat breast cancer. AAU68525-148617 represent protein
 CC fragments encoded by the expressed sequence tags described in the method
 CC of the invention
 XX
 SQ Sequence 195 AA;
 Query Match 100.0%; Score 378; DB 2; Length 195;
 Best Local Similarity 100.0%; Pred. No. 3.7e-40;
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLHFIDQHRALIAIARVTVNVEWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSTPAWN 60

Db 111 GLHFIDQHRALIAIARVTVNVEWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSTPAWN 170
 QY 61 WTCKDLLLQAL 71
 DB 171 WTCKDLLLQAL 181
 RESULT 3
 AAU68525
 ID AAU68525 standard; protein; 195 AA.
 AC AAU68525;
 DT 16-JAN-2002 (first entry)
 DE Human novel cytokine encoded by cDNA 790CIP2B_1 #1.
 KW Human; cytokine; cell proliferation; cell differentiation;
 KW antiinflammatory; stem cell growth factor; activin; inhibin; cancer;
 KW nervous system disease; neuropathy; Alzheimer's disease;
 KW Parkinson's disease; Huntington's disease; spinal cord disorder;
 KW head trauma; stroke; myeloid cell disorder; lymphoid cell disorder;
 KW platelet disorder; tissue regeneration; wound healing; ulcer;
 KW aplastic anaemia; osteoarthritis; bone degenerative disorder;
 KW osteoporosis; fibrosis; reperfusion; immune disorder; SCID;
 KW periodontal disease; infection; autoimmune disorder;
 KW severe combined immunodeficiency; infection; diabetes mellitus; allergy;
 KW multiple sclerosis; rheumatoid arthritis; sepsis; nephritis;
 KW asthma; coagulation disorder; haemophilia; food supplement; immunogen.
 KW inflammatory bowel disease; immunogen.
 XX Homo sapiens.
 OS
 PN WO200175093-A1.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US010484.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 PR 22-SEP-2000; 2000US-00668680.
 PR 23-OCT-2000; 2000US-00655618.
 PR 30-NOV-2000; 2000US-00728711.
 PR 14-MAR-2001; 2001US-00808701.
 XX (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;
 PI Xu C, Yang Y, Zhao QA, Chen R, Wang D, Goodrich RW, Liu C;
 PI Drmanac RT;
 XX
 DR WPI; 2001-626432/72.
 DR N-PSDB; AAS59817.
 XX
 PS New polypeptides and nucleic acids, useful for diagnosis, treatment of
 PS inflammatory, autoimmune, neurological, myeloid or lymphoid cell, bone
 PS degenerative disorders, cancer and promoting wound healing.
 XX
 PS Claim 20; Page 242-243; 336pp; English.
 XX
 CC The invention relates to isolated human polypeptides (which may be
 CC cytokines) and the polynucleotides encoding them. The protein is useful
 CC for identifying a compound which binds to it (e.g. modulators, agonists
 CC and antagonists). The polynucleotides are useful as an array for mismatch
 CC detection. The proteins and nucleic acids are useful as nutritional
 CC sources or supplements. The protein exhibits activity relating
 CC to cytokine, cell proliferation, cell differentiation, antiinflammatory,
 CC stem cell growth factor activity, immune stimulating or immune
 CC suppressing and activin or inhibin related activities. The proteins (and
 CC antibodies raised against them) and nucleic acids are therefore useful in
 CC the diagnosis and treatment of diseases and disorders such as cancer,
 CC central and peripheral nervous system diseases and neuropathies,

Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, spinal cord disorders, head trauma, cerebrovascular diseases, strokes, myeloid and lymphoid cell disorders, platelet disorders, thrombocytopaenias, stem cell disorders, aplastic anaemia, for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders (e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis), allergic reactions and conditions, such as asthma or other respiratory problems, coagulation disorders, haemophilia), septic shock, sepsis, arthritis, nephritis and inflammatory bowel disease, viral infection and are useful in altering bodily characteristics. The present sequence represents a novel protein of the invention

Sequence 195 AA:
XX
XX

Query Match 100.0%; Score 378; DB 4; Length 195;
Best Local Similarity 100.0%; Pred. No. 3.7e-40;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

RESULT 4
AAB20085
ID AAB20085 standard; protein; 195 AA.

AAB20085;
23-APR-2001 (first entry)

Human CARD-5 protein.

CARD-5; caspase recruitment domain; human; cancer; infection; autoimmune disease; neurological disease; haematological disease; immune disease; inflammation; antitumour; anesthetic; immunomodulator; antiinflammatory; apoptosis; diagnosis; gene therapy.

Homo sapiens.

key	Location/Qualifiers
Domain	111. .181
	/note= "CARD"

WO200100826-A2.

04-JAN-2001.

28-JUN-2000; 2000WO-US017691.

28-JUN-1999; 99US-00340620.

(MILL-) MILLENNIUM PHARM INC.

Bertin J;

WPI; 2001-061973/07.

XX
N-PSDB; HAF30007.

isolated intracellular proteins predicted to be involved in regulating caspase activation are used for diagnosis and treatment of e.g. cancer, viral infections, autoimmune diseases, neurological diseases and hematological disorders.

[illegible]

Claim 9; Fig 21; 208pp; English.

The present sequence is that of human caspase recruitment domain 5 (CARD-5), an intracellular protein predicted to be involved in regulating caspase activation. The sequence is predicted from an isolated cDNA clone (see AAP00007). Methods of diagnosing and treating patients suffering from a disorder associated with an abnormal level or rate of apoptotic cell death, abnormal activity of the Fas/Apo-1 receptor complex, abnormal activity of the tumour necrosis factor receptor complex or abnormal activity of a caspase involve administering a compound that modulates the expression or activity of CARD-3, CARD-4, CARD-5 or CARD-6 e.g. using gene therapy methods. Such disorders include cancer, viral infection, autoimmune disorders, neurological diseases, haematological disorders, inflammatory disorders and immune disorders. CARD-3, -4, -5 and -6 proteins can be used to regulate cell proliferation, cell survival and cell growth. They can also be used to screen drugs or compounds that modulate their activity or expression and to treat disorders associated with insufficient or excessive production of CARD-3, -4, -5 or -6 protein, or production of an aberrant protein.

Sequence 195 AA;

Query Match	100.0%;	Score 378;	DB 4;	Length 195;
Best Local Similarity	100.0%;	Pred. No. 3.7e-40;		
Matches	71:	Conservative	0:	Mismatches 0: Indels

1	GLHFIDQRAALIA	RVTNVSWLLD	ALYKVLTD	EQYQAVRAEPTNP	SKMRKLFSTPAWN	60
111	GLHFIDQRAALIA	RVTNVSWLLD	ALYKVLTD	EQYQAVRAEPTNP	SKMRKLFSTPAWN	170
61	WTCRDL	LLQAL	71			
171	WTCRDL	LLQAL	181			

RESULT 5

AAE000388
ID AAE00588 standard; protein; 195 AA.

AA
AC
AAE00588;

02-JUL-2001 (first entry)

Human target of methylation-induced silencing-1 (TMS1) protein.

XX Human; target of methylation-induced silencing-1; TMS1; cytostatic;
KW antiproliferative; apoptosis inducer; gene therapy; CpG island;
KW caspase-recruiting domain; CARD; cancer; breast.

XX
OS
Homo sapiens.XX
PN
WQ200129235-A2XX
PD
26-APR-2001XX
DE
18-OCT-2000.

XX
18-OCT-1999. 0011S-015007ED
DP

XX
PA
(ITEM) 1 1111 11000

XXIX

XX

DR N-PSDB; AAD03889, AAD03890.

Novel gene TMS1, transcriptionally silenced due to increased methylation useful for identifying subject at risk of developing tumor characterized by abnormal methylation, for treating cancer by inducing apoptosis.

PS
xx
Claim 85; Page 114; 124pp; English.

The invention relates to identification of target of methylation-induced silencing-1 (TMS1) gene. This gene is transcriptionally silenced due to abnormal methylation of a CpG island in its 5' regulatory region. TMS1 consists of a carboxy terminal caspase-recruiting domain (CARD) and plays a role in induction of apoptosis. TMS1 gene and protein are useful as tools for diagnosing and treating a subject at risk of developing cancer (e.g. breast cancer) characterised by abnormal CpG methylation or abnormally low levels of TMS1 expression products. Unique fragments of TMS1 gene are also used as probes. TMS1 gene is useful in gene therapy. TMS1 molecule is also useful for treating abnormal cell proliferation by increasing TMS1 polypeptide level to an above normal level. The CpG island region of TMS1 or its fragments are used to study the methylation patterns apart from any coding region contained in it. The present sequence is human target of methylation-induced silencing-1 (TMS1) protein

Sequence 195 AA;

Sequence 195 AA;

Query March	100.0%;	Score 378;	DB 4;	Length 195;
Best Local Similarity	100.0%;	Pred. No 3.7e-40;		
Matches 71;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
1	GLHFIDQRAALIAI	RVINVEWLLDALY	KGKVLTD	EYQAVRAEPTNP
				SKRKLFSFTPAWN
111	GLHFIDQRAALIAI	RVINVEWLLDALY	KGKVLTD	EYQAVRAEPTNP
				SKRKLFSFTPAWN
61	WTCKDLLLQAL	71		
171	WTCKDLLLQAL	181		

RESULT 6

AAU99353
ID AAU99353 standard; protein: 195 AA.

AA
AC - AAU99353;

AA	07-OCT-2002	(first entry)
DT		

XX DE Human caspase recruitment domain-5 (CARD-5) protein.

WPI; 2002-557538/59.
N-PSDB: ABK87966

Novel isolated murine or human caspase recruitment domain (CARD)-5 polypeptide, useful for treating immune disorders such as Hashimoto's thyroiditis, graft rejection, allergy, glomerular nephritis, tuberculosis.

Claim 22: Fig 3: 100pp; English.

The invention discloses the isolated polypeptides, and encoding nucleic acids, of murine and human caspase recruitment domain (CARD)-5. Caspases (cysteinyl aspartate-specific proteinases) are central to the apoptotic program and responsible for the degradation of cellular proteins that lead to the morphological changes seen in cells undergoing apoptosis. Caspases interact with other caspases via their CARDs and different subtypes of CARDs may confer binding specificity. CARD-5 is an intracellular protein that is predicted to be involved in regulating caspase activation. CARD-5 activates the nuclear factor-kappa B (NF-kappaB) transcription factor pathway and binds the CARDs of caspase-1, NF-CARD-7 and itself. CARD-5 can, therefore, modulate CARD-5 activity and NF-kappaB activation, regulate cell growth and cell death and be used in gene therapy. The CARD-5 polypeptides are useful for identifying compounds which bind to them and modulate their activity and for detecting the presence of CARD-5 in a sample. CARD-5 polypeptides, nucleic acids, antibodies and modulators of CARD-5 expression or activity can be used to treat immune disorders such as chronic inflammatory diseases and disorders, Hashimoto's thyroiditis, graft rejection, sarcoidosis, atopic conditions (such as asthma and allergy), glomerular nephritis, human immunodeficiency virus (HIV) and bacterial infections (including tuberculosis and lepromatous leprosy) and in screening and detection assays. Modulators of CARD-5 activity or expression are also useful for treating autoimmune disorders, such as systemic lupus erythematosus and arthritis, cell depletion, neurological disorders, such as Alzheimer's disease, Parkinson's disease and spinal muscular atrophy, haematologic diseases, such as myelodysplastic syndrome and aplastic anaemia, myocardial infarction and stroke. The sequence presented is the human caspase recruitment domain-5 (CARD-5) protein

Sequence 195 AA:

```

Query Match      100.0%; Score 378; DB 5; Length 195;
Best Local Similarity 100.0%; Pred. No. 3.7e-40;
Matches 71: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 7

AAO17854
ID AAO17854 standard: protein: 195 AA.

XX
AC
AAO17854:XX
DT 20-AUG-2002 (first entry)[illegible]

XX AC AAG74647;
 XX DT 03-SEP-2001 (first entry)
 XX DE Human colon cancer antigen protein SEQ ID NO:5411.
 XX KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
 XX KW colorectal carcinoma.
 XX OS Homo sapiens.
 XX PN WO200122920-A2.
 XX PD 05-APR-2001.
 XX PF 28-SEP-2000; 2000WO-US026524.
 XX PR 29-SEP-1999; 99US-0157137P.
 XX PR 03-NOV-1999; 99US-0163280P.
 XX PR (HUMA-) HUMAN GENOME SCI INC.
 XX PA Ruben SM, Barash SC, Birse CE, Rosen CA;
 XX PI WPI; 2001-235357/24.
 XX DE N-PSDB; AAH34052.
 XX PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 XX PT useful for preventing, diagnosing and/or treating colorectal cancers.
 XX PS Claim 11; Page 7035-7036; 9803pp; English.
 XX CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
 CC proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene therapy
 CC and vaccine production. N and P may be used in the prevention, diagnosis
 CC and treatment of diseases associated with inappropriate P expression. For
 CC example, N and P may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of P by expressing inactive proteins or to
 CC supplement the patients own production of P. Additionally, N may be used
 CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
 CC into a host cell and culturing the cell to express the proteins. N and P
 CC can be used in the prevention, diagnosis and treatment of colorectal
 CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
 CC sequences used in the exemplification of the present invention. N.B.
 CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
 CC time of publication, meaning no sequences are present for SEQ ID NO:1027
 CC to 1052, 7921 and 7922
 XX SQ Sequence 205 AA;
 XX Query Match 100.0%; Score 378; DB 4; Length 205;
 XX Best Local Similarity 100.0%; Pred. No. 3.9e-40; Indels 0; Gaps 0;
 XX Matches 71; Conservative 0; Mismatches 0;
 XX 1 GLHFDQHRAALIAIARVTNVVWLLDALYGVLTDEQVAVRAEPTNPSKMKLFSTPAWN 60
 XX 121 GLHFDQHRAALIAIARVTNVVWLLDALYGVLTDEQVAVRAEPTNPSKMKLFSTPAWN 180
 XX 61 WTKDILLQAL 71
 XX 181 WTKDILLQAL 191
 XX RESULT 10
 XX AAE00591
 XX ID AAE00591 standard; protein; 84 AA.
 XX AC
 XX AC AAE00591;
 XX XX

DT 02-JUL-2001 (first entry)
 XX DE Human target of methylation-induced silencing-1 (TMS1) exon3 protein.
 XX KW Human; target of methylation-induced silencing-1; TMS1; cytostatic;
 XX KW antiproliferative; apoptosis inducer; gene therapy; CpG island;
 XX KW caspase-recruiting domain; CARD; cancer; breast.
 XX OS Homo sapiens.
 XX PN WO200129235-A2.
 XX PD 26-APR-2001.
 XX PF 18-OCT-2000; 2000WO-US028747.
 XX PR 18-OCT-1999; 99US-0159975P.
 XX PR (UYEM-) UNIV EMORY.
 XX PI Vertino PM;
 XX DR WPI; 2001-290922/30.
 XX DR N-PSDB; AAD03894.
 XX PT Novel gene TMS1, transcriptionally silenced due to increased methylation
 XX PT useful for identifying subject at risk of developing tumor characterized
 XX PT by abnormal methylation, for treating cancer by inducing apoptosis.
 XX PS Claim 25; Page 117; 124pp; English.
 XX CC The invention relates to identification of target of methylation-induced
 CC silencing-1 (TMS1) gene. This gene is transcriptionally silenced due to
 CC abnormal methylation of a CpG island in its 5' regulatory region. TMS1
 CC consists of a carboxy terminal caspase-recruiting domain (CARD) and plays
 CC a role in induction of apoptosis. TMS1 gene and protein are useful as
 CC tools for diagnosing and treating a subject at risk of developing cancer
 CC (e.g. breast cancer) characterised by abnormal CpG methylation or
 CC abnormally low levels of TMS1 expression products. Unique fragments of
 CC TMS1 gene are also useful as probes. TMS1 gene is useful in gene therapy. TMS1
 CC molecule is also useful for treating abnormal cell proliferation by
 CC increasing TMS1 polypeptide level to an above normal level. The CpG
 CC island region of TMS1 or its fragments are used to study the methylation
 CC patterns apart from any coding region contained in it. The present
 CC sequence is human target of methylation-induced silencing-1 (TMS1) exon3
 XX protein
 XX SQ Sequence 84 AA;
 XX Query Match 98.4%; Score 372; DB 4; Length 84;
 XX Best Local Similarity 100.0%; Pred. No. 7.5e-40;
 XX Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX 2 LHFIDQHRAALIAIARVTNVVWLLDALYGVLTDEQVAVRAEPTNPSKMKLFSTPAWN 61
 XX 1 LHFIDQHRAALIAIARVTNVVWLLDALYGVLTDEQVAVRAEPTNPSKMKLFSTPAWN 60
 XX 62 TCKDILLQAL 71
 XX 61 TCKDILLQAL 70
 XX RESULT 11
 XX AAE00593
 XX ID AAE00593 standard; protein; 171 AA.
 XX AC
 XX AC AAE00593;
 XX DT 02-JUL-2001 (first entry)
 XX DE Rat target of methylation-induced silencing-1 (TMS1) partial protein.
 XX KW Rat; target of methylation-induced silencing-1; TMS1; cytostatic;

Qy	3	HFIDQRAALIAIRVTVNVEWLDALYGVKLTDEQYQAVRAEPTNFSKVRKULFSFTPAWNT	62
Db	111	HFVDQRQALIAIRVTEVDGLDAGSLVTEGQYQAVRAETTSQDKMRKULFSFVPSWNL	70
Qy	63	CKDLILQAL	71
Db	171	CKDSLQAL	179
RESULT 15			
AAB24513	ID	AAB24513 standard; protein; 442 AA.	
XX	AC	AAB24513;	
XX	DT	20-NOV-2000 (first entry)	
XX	DE	Human secreted protein sequence encoded by gene 12 SEQ ID NO:139.	
XX	KW	Human; secreted protein; cytostatic; antianaemic; antidiabetic;	
XX	KW	antiinflammatory; ophthalmological; antirheumatic; antiarthritic;	
XX	KW	antipsoriatic; antiangiogenic; cardiant; anti-HIV; nootropic;	
XX	KW	neuroprotective; antimicrobial; antiparkinsonian; cancer;	
XX	KW	immune system disorder; angiogenesis; hyperproliferative disorder;	
XX	KW	cardiovascular disorder; apoptosis; neurological disease;	
XX	KW	infectious disease; wound healing.	
XX	OS	Homo sapiens.	
XX	PN	WC0200035937-A1.	
XX	PD	22-JUN-2000.	
XX	PF	16-DEC-1999; 99WO-US029950.	
XX	PR	17-DEC-1998; 98US-0112809P.	
XX	PR	18-DEC-1998; 98US-0113006P.	
XX	PA	(HUMA-) HUMAN GENOME SCI INC.	
XX	PI	Ruben SM, Ebner R, Rosen CA, Endress GA, Soppet DR, Ni J;	
XX	PI	Duan DR, Moore PA, Shi Y, Lafleur DW, Olsen HS, Florence K;	
XX	DR	WPI; 2000-431566/37.	
XX	PT	Forty seven human nucleic acids encoding secreted proteins, useful in the	
XX	PT	treatment, prevention and diagnosis of cancers, disorders of the immune	
XX	PT	system, angiogenesis disorders, neurological diseases and	
XX	PT	hyperproliferative disorders.	
XX	PS	Disclosure; Page 37; 562pp; English.	
XX	CC	The polynucleotide sequence given in AAB78381 to AAB78432 encode the	
XX	CC	human secreted proteins given in AAB24437 to AAB24604. Human secreted	
XX	CC	proteins have activities based on the tissues and cells the genes are	
XX	CC	expressed in. Examples of activities include: cytostatic; antianaemic;	
XX	CC	antidiabetic; antiinflammatory; ophthalmological; antirheumatic;	
XX	CC	antiarthritic; antipsoriatic; antiangiogenic; cardiant; anti-HIV;	
XX	CC	nootropic; neuroprotective; antimicrobial and antiparkinsonian. Human	
XX	CC	secreted protein polynucleotides, polypeptides, antagonists and/or	
XX	CC	agonists may be useful in treating, preventing, and/or diagnosing other	
XX	CC	diseases, disorders, and/or conditions such as: (a) cancers; (b)	
XX	CC	disorders of the immune system; (c) angiogenesis disorders; (d)	
XX	CC	hyperproliferative disorders; (e) cardiovascular disorders; (f) diseases	
XX	CC	associated with increase apoptosis; (g) neurological diseases; and (h)	
XX	CC	infectious diseases. They are also used to promote wound healing.	
XX	CC	AAA78372 to AAB78380. and AAB24436 represent sequences used in the	
XX	CC	exemplification of the present invention	
XX	QQ	Sequence 442 AA;	

```
Best Local Similarity    61.4%, Pred.No. 6.8e-19;
Matches   43; Conservative      12; Mismatches   15; Indels       0; Gaps     0;
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QY	2	LHFIDQHRAALIAIARTVTNVVLLDALYGKVLTDGYYQAVRAEPTNPSKMRLFSFPAWNW	61
		: : : : : : : : :	
Db	339	LHFDVGYREQLIARVTSVEVVLDKLHGQVLSQEGYERVALENTSPSQMKLFSLSQSMDR	398
		: : : : : : : : :	
QY	62	TCKDLLIQAL	71
Db	399	KCKDGLYQAL	408

Search completed: July 28, 2004, 08:53:00
Job time : 41.0602 secs



GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 28, 2004, 08:51:17 ; Search time 12.4036 seconds
(without alignments)
295.514 Million cell updates/sec

Title: US-09-996-617-8_COPY_111_181
Perfect score: 378
Sequence: 1 GLHFIDQHRAALIAIARVTNVE.....LFSFTPAWNTCKLLIQLAL 71

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pcp.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pcp.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pcp.*
5: /cgn2_6/ptodata/2/iaa/PCUTS COMB.pcp.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	378	100.0	71	4	US-09-340-620A-58
2	378	100.0	195	4	US-09-340-620A-49
3	264	69.8	70	4	US-09-340-620A-57
4	264	69.8	70	4	US-09-340-620A-66
5	264	69.8	193	4	US-09-340-620A-61
6	130.5	34.5	109	4	US-09-340-620A-71
7	69.5	18.4	106	4	US-09-069-023-10
8	69.5	18.4	208	4	US-09-069-023-8
9	69.5	18.4	221	4	US-09-069-023-22
10	65.5	17.3	94	4	US-09-099-041A-31
11	65.5	17.3	94	4	US-09-245-281-31
12	65.5	17.3	94	4	US-09-207-359B-31
13	65.5	17.3	94	4	US-09-340-620A-31
14	65.5	17.3	94	4	US-09-865-364-31
15	64.5	17.1	100	4	US-09-099-041A-10
16	64.5	17.1	100	4	US-09-245-281-10
17	64.5	17.1	100	4	US-09-207-359B-10
18	64.5	17.1	100	4	US-09-340-620A-10
19	64.5	17.1	100	4	US-09-865-364-10
20	64.5	17.1	164	4	US-09-245-281-41
21	64.5	17.1	164	4	US-09-207-359B-41
22	64.5	17.1	164	4	US-09-340-620A-41
23	64.5	17.1	164	4	US-09-865-364-41
24	64.5	17.1	249	4	US-09-245-281-39
25	64.5	17.1	249	4	US-09-207-359B-39
26	64.5	17.1	249	4	US-09-340-620A-39
27	64.5	17.1	249	4	US-09-865-364-39

28	64.5	17.1	409	4	US-09-207-359B-46	Sequence 46, Appl
29	64.5	17.1	409	4	US-09-865-364-46	Sequence 46, Appl
30	64.5	17.1	953	4	US-09-099-041A-8	Sequence 8, Appl
31	64.5	17.1	953	4	US-09-245-281-8	Sequence 8, Appl
32	64.5	17.1	953	4	US-09-207-359B-8	Sequence 8, Appl
33	64.5	17.1	953	4	US-09-340-620A-8	Sequence 8, Appl
34	64.5	17.1	953	4	US-09-865-364-8	Sequence 8, Appl
35	62.5	16.5	109	4	US-09-099-041A-6	Sequence 6, Appl
36	62.5	16.5	109	4	US-09-245-281-6	Sequence 6, Appl
37	62.5	16.5	109	4	US-09-340-620A-6	Sequence 6, Appl
38	62.5	16.5	110	4	US-09-207-359B-6	Sequence 6, Appl
39	62.5	16.5	110	4	US-09-865-364-6	Sequence 6, Appl
40	62.5	16.5	167	4	US-09-069-023-6	Sequence 6, Appl
41	62.5	16.5	284	4	US-09-069-023-5	Sequence 5, Appl
42	62.5	16.5	478	4	US-09-069-023-4	Sequence 4, Appl
43	62.5	16.5	530	4	US-09-069-023-3	Sequence 3, Appl
44	62.5	16.5	531	4	US-09-069-023-1	Sequence 1, Appl
45	62.5	16.5	540	3	US-09-019-942-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-340-620A-58
; Sequence 58, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340,620A
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-340-620A-58

Query Match	100.0%	Score 378	DB 4	Length 71
Best Local Similarity	100.0%	Pred.No.1.5e-42	Mismatches 0	Indels 0
Matches	71	Conservative	0	Gaps 0
QY	1	GLHFIDQHRAALIAIARVTNVEWLLDALYGVKLTDEQYQAVRAEPTNPSKORXLFSTPAWN	60	
Db	1	GLHFIDQHRAALIAIARVTNVEWLLDALYGVKLTDEQYQAVRAEPTNPSKORXLFSTPAWN	60	
QY	61	WTCKLLIQLAL	71	
Db	61	WTCKLLIQLAL	71	

RESULT 2
US-09-340-620A-49
; Sequence 49, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340,620A
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281

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; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-340-620A-49

Query Match      100.0%; Score 378; DB 4; Length 195;
Best Local Similarity 100.0%; Pred. No. 5.4e-42;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFDQRAALIAARVTNVVWLLDALYKGLTDEQYQAVRAEPTNPSKMKLFSTPAWN 60
Db 111 GLHFDQRAALIAARVTNVVWLLDALYKGLTDEQYQAVRAEPTNPSKMKLFSTPAWN 170

QY 61 WTKDILLQAL 71
Db 171 WTKDILLQAL 181

RESULT 3
US-09-340-620A-57
; Sequence 57, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340,620A
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-340-620A-57

Query Match      69.8%; Score 264; DB 4; Length 70;
Best Local Similarity 73.9%; Pred. No. 1.6e-27;
Matches 51; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 3 HFIDQRAALIAARVTNVVWLLDALYKGLTDEQYQAVRAEPTNPSKMKLFSTPAWN 62
Db 2 HFVDQRAALIAARVTNVVWLLDALHGSVLTGQYQAVRAETSDQKMKLFSTPAWN 61

QY 63 CKDILLQAL 71
Db 62 CKDILLQAL 70

RESULT 4
US-09-340-620A-66
; Sequence 66, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
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; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340,620A
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-340-620A-66

Query Match      69.8%; Score 264; DB 4; Length 70;
Best Local Similarity 73.9%; Pred. No. 1.6e-27;
Matches 51; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 3 HFIDQRAALIAARVTNVVWLLDALYKGLTDEQYQAVRAEPTNPSKMKLFSTPAWN 62
Db 2 HFVDQRAALIAARVTNVVWLLDALHGSVLTGQYQAVRAETSDQKMKLFSTPAWN 61

QY 63 CKDILLQAL 71
Db 62 CKDILLQAL 70

RESULT 5
US-09-340-620A-61
; Sequence 61, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340,620A
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-340-620A-61

Query Match      69.8%; Score 264; DB 4; Length 193;
Best Local Similarity 73.9%; Pred. No. 5.7e-27;
Matches 51; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 3 HFIDQRAALIAARVTNVVWLLDALYKGLTDEQYQAVRAEPTNPSKMKLFSTPAWN 62
Db 111 HFVDQRAALIAARVTNVVWLLDALHGSVLTGQYQAVRAETSDQKMKLFSTPAWN 170

QY 63 CKDILLQAL 71
Db 171 CKDILLQAL 179

RESULT 6
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US-09-340-620A-71
; Sequence 71, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340,620A
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence
; NAME/KEY: VARIANT
; LOCATION: (1)...(109)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-340-620A-71

Query Match 34.5%; Score 130.5; DB 4; Length 109;
Best Local Similarity 47.4%; Pred. No. 1.1e-09;
Matches 37; Conservative 10; Mismatches 24; Indels 7; Gaps 4;

QY 1 GLHFIDQHRALRIARVTN--VEWLLDALYK-VLTDEQYQAVRAEPTNPSKMKLFSTFP 57
DB 7 GSEIIDQHRXALLIARVTEDPXDLLDALLSRDLISEDYENAEVETTLXSKYRKLLILVQ 66

QY 58 A-WNWTCKDL---LLQAL 71
DB 67 SKGEETCKXFLKCLLQAL 84

RESULT 7
US-09-069-023-10
; Sequence 10, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-10

Query Match 18.4%; Score 69.5; DB 4; Length 106;
Best Local Similarity 26.8%; Pred. No. 0.12; Indels 25; Gaps 3;
Matches 22; Conservative 12; Mismatches 23;

QY 5 IDQHRALRIARV-TNVEWLLDALYK-VLTDEQYQAVRAEPTNPSKMKLFSTFP----- 56
DB 12 IDREKRLVETLQADSGLLDALLARGVLTGPEYEALDLPDAERRVRLLLLVQKGEA 71

QY 57 -----PANW 61

Db 72 ACQELLRCQAORTAGAPDPADW 93
|||:|
RESULT 8
US-09-069-023-8
; Sequence 8, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-8

Query Match 18.4%; Score 69.5; DB 4; Length 208;
Best Local Similarity 26.8%; Pred. No. 0.28; Indels 25; Gaps 3;
Matches 22; Conservative 12; Mismatches 23;

QY 5 IDQHRALRIARV-TNVEWLLDALYK-VLTDEQYQAVRAEPTNPSKMKLFSTFP----- 56
DB 12 IDREKRLVETLQADSGLLDALLARGVLTGPEYEALDLPDAERRVRLLLLVQKGEA 71

QY 57 -----PANW 61
Db 72 ACQELLRCQAORTAGAPDPADW 93
|||:|
RESULT 9
US-09-069-023-22
; Sequence 22, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-069-023-22

Query Match 18.4%; Score 69.5; DB 4; Length 221;
Best Local Similarity 26.8%; Pred. No. 0.3; Indels 25; Gaps 3;
Matches 22; Conservative 12; Mismatches 23;

QY 5 IDQHRALRIARV-TNVEWLLDALYK-VLTDEQYQAVRAEPTNPSKMKLFSTFP----- 56
DB 12 IDREKRLVETLQADSGLLDALLARGVLTGPEYEALDLPDAERRVRLLLLVQKGEA 71

QY 57 -----PANW 61
Db 72 ACQELLRCQAORTVSMFDPADW 93
|||:|
RESULT 10

US-09-099-041A-31
; Sequence 31, Application US/09099041A
; Patent No. 6340576
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/09/099,041A
; CURRENT FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-099-041A-31

Query Match 17.3%; Score 65.5; DB 4; Length 94;
Best Local Similarity 25.9%; Pred. No. 0.34;
Matches 21; Conservative 12; Mismatches 23; Indels 25; Gaps 3;
QY 6 DQHRAALIARV-TNVEWLLDALYCK-VLTDEQYQAVRAEPTNPSKMKLFSFT-----56
Db 10 DRERKRLVETLQADSGLLLDALLARGVLTGPEYEALDLPDAERRVRLILLVQKGGEAA 69
QY 57 -----PAWNW 61
Db 70 CQELLRCQRTAGAPDPADW 90

RESULT 11
US-09-245-281-31
; Sequence 31, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/09/245,281
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: US 09/207,359
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 09/099,041
; EARLIER FILING DATE: 1998-06-17
; EARLIER APPLICATION NUMBER: US 09/019,942
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-245-281-31

Query Match 17.3%; Score 65.5; DB 4; Length 94;
Best Local Similarity 25.9%; Pred. No. 0.34;
Matches 21; Conservative 12; Mismatches 23; Indels 25; Gaps 3;
QY 6 DQHRAALIARV-TNVEWLLDALYCK-VLTDEQYQAVRAEPTNPSKMKLFSFT-----56
Db 10 DRERKRLVETLQADSGLLLDALLARGVLTGPEYEALDLPDAERRVRLILLVQKGGEAA 69
QY 57 -----PAWNW 61
Db 70 CQELLRCQRTAGAPDPADW 90

RESULT 12
US-09-207-359B-31

; Sequence 31, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/207,359B
; CURRENT FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-207-359B-31

Query Match 17.3%; Score 65.5; DB 4; Length 94;
Best Local Similarity 25.9%; Pred. No. 0.34;
Matches 21; Conservative 12; Mismatches 23; Indels 25; Gaps 3;
QY 6 DQHRAALIARV-TNVEWLLDALYCK-VLTDEQYQAVRAEPTNPSKMKLFSFT-----56
Db 10 DRERKRLVETLQADSGLLLDALLARGVLTGPEYEALDLPDAERRVRLILLVQKGGEAA 69
QY 57 -----PAWNW 61
Db 70 CQELLRCQRTAGAPDPADW 90

RESULT 13
US-09-340-620A-31
; Sequence 31, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340,620A
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-340-620A-31

Query Match 17.3%; Score 65.5; DB 4; Length 94;
Best Local Similarity 25.9%; Pred. No. 0.34;
Matches 21; Conservative 12; Mismatches 23; Indels 25; Gaps 3;
QY 6 DQHRAALIARV-TNVEWLLDALYCK-VLTDEQYQAVRAEPTNPSKMKLFSFT-----56
Db 10 DRERKRLVETLQADSGLLLDALLARGVLTGPEYEALDLPDAERRVRLILLVQKGGEAA 69
QY 57 -----PAWNW 61
Db 70 CQELLRCQRTAGAPDPADW 90

Search completed: July 28, 2004, 08:55:58
Job time : 12.4036 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2004, 08:54:53 ; Search time 34.6446 Seconds
(without alignments)

642.856 Million cell updates/sec

Title: US-09-996-617-8_COPY_111_181

Perfect score: 378

sequence: 1 GLHFIDQHRALIAITVNE.....LFSFTPAWNTCKDLLQAL 71

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 segs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	378	100.0	71	9	US-09-728-721-58
2	378	100.0	71	14	US-10-295-981-58
3	378	100.0	85	9	US-09-841-879B-8
4	378	100.0	85	16	US-10-756-097-8
5	378	100.0	90	9	US-09-931-071-7
6	378	100.0	195	9	US-09-728-721-49
7	378	100.0	195	9	US-09-996-617-8
8	378	100.0	195	9	US-09-841-879B-5
9	378	100.0	195	12	US-10-446-046-4
10	378	100.0	195	14	US-10-295-981-49
11	378	100.0	195	15	US-10-240-145-55
12	378	100.0	195	15	US-10-131-410-84
13	378	100.0	195	16	US-10-756-097-5
14	378	100.0	205	14	US-10-106-698-5421
15	269	71.2	85	9	US-09-841-879B-15

16	269	71.2	85	16	US-10-756-097-15	Sequence 15, Appl
17	264	69.8	70	9	US-09-728-721-57	Sequence 57, Appl
18	264	69.8	70	9	US-09-728-721-66	Sequence 66, Appl
19	264	69.8	70	14	US-10-295-981-57	Sequence 57, Appl
20	264	69.8	70	14	US-10-295-981-66	Sequence 66, Appl
21	264	69.8	84	9	US-09-841-879B-7	Sequence 7, Appl
22	264	69.8	84	16	US-10-756-097-7	Sequence 7, Appl
23	264	69.8	193	9	US-09-728-721-61	Sequence 61, Appl
24	264	69.8	193	9	US-09-841-879B-2	Sequence 2, Appl
25	264	69.8	193	14	US-10-295-981-61	Sequence 61, Appl
26	264	69.8	193	16	US-10-756-097-2	Sequence 2, Appl
27	216	57.1	88	9	US-09-841-739-15	Sequence 15, Appl
28	216	57.1	88	14	US-10-449-315-15	Sequence 15, Appl
29	216	57.1	442	10	US-09-895-298-139	Sequence 139, Appl
30	216	57.1	1399	9	US-09-388-221-4	Sequence 4, Appl
31	216	57.1	1429	9	US-09-996-617-2	Sequence 2, Appl
32	216	57.1	1429	9	US-09-931-071-2	Sequence 3, Appl
33	216	57.1	1429	12	US-10-029-347-3	Sequence 26, Appl
34	216	57.1	1429	12	US-10-029-347-26	Sequence 11, Appl
35	216	57.1	1429	14	US-10-028-392-11	Sequence 3, Appl
36	216	57.1	1429	14	US-10-028-374-3	Sequence 15, Appl
37	216	57.1	1429	14	US-10-028-374-15	Sequence 3, Appl
38	216	57.1	1429	14	US-10-183-770-3	Sequence 15, Appl
39	216	57.1	1429	14	US-10-183-770-15	Sequence 6, Appl
40	216	57.1	1443	9	US-09-388-221-6	Sequence 2, Appl
41	216	57.1	1473	9	US-09-388-221-2	Sequence 8, Appl
42	216	57.1	1473	12	US-10-182-822A-8	Sequence 5422, Ap
43	214	56.6	158	14	US-10-106-698-5422	Sequence 1120, Ap
44	214	56.6	190	9	US-09-925-301-1120	Sequence 145, App
45	141	37.3	65	10	US-09-895-298-145	

ALIGNMENTS

RESULT 1
US-09-728-721-58
; Sequence 58, Application US/09728721
; Patent No US20020061845A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/728,721
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-728-721-58

Query Match	100.0%;	Score 378;	DB 9;	Length 71;
Best Local Similarity	100.0%;	Pred. NO. 5.6e-40;		
Matches	71;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;
QY	1	GLHFIDQHRALIAITVNEVLLDLYGKVLDEQYQAVRAEPTNPFSKMKLFSTPAWN	60	
Db	1	GLHFIDQHRALIAITVNEVLLDLYGKVLDEQYQAVRAEPTNPFSKMKLFSTPAWN	60	
QY	61	WTCKLLQAL	71	
Db	61	WTCKLLQAL	71	

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RESULT 2
US-10-295-981-58
; Sequence 58, Application US/10295981
; Publication No. US20030120055A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/10/295,981
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-981-58

Query Match      100.0%; Score 378; DB 14; Length 71;
Best Local Similarity 100.0%; Pred. No. 5.6e-40;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFDQHRALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSSKMKLFSFTPAWN 60
DB 1 GLHFDQHRALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSSKMKLFSFTPAWN 60
QY 61 WTCKDLLLQAL 71
DB 61 WTCKDLLLQAL 71

RESULT 3
US-09-841-879B-8
; Sequence 8, Application US/09841879B
; Patent No. US20020142979A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-330001
; CURRENT APPLICATION NUMBER: US/09/841,879B
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 09/728,721
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/340,620
; PRIOR FILING DATE: 1999-06-28
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-841-879B-8

Query Match      100.0%; Score 378; DB 9; Length 85;
Best Local Similarity 100.0%; Pred. No. 6.9e-40;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFDQHRALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSSKMKLFSFTPAWN 60
DB 1 GLHFDQHRALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSSKMKLFSFTPAWN 60
QY 61 WTCKDLLLQAL 71
DB 61 WTCKDLLLQAL 71

RESULT 4
US-10-756-097-8
; Sequence 8, Application US/10756097
; Publication No. US20040127685A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND
; FILE REFERENCE: 07334-330001
; CURRENT APPLICATION NUMBER: US/10/756,097
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: US/09/841,879B
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 09/728,721
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/340,620
; PRIOR FILING DATE: 1999-06-28
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-756-097-8

Query Match      100.0%; Score 378; DB 16; Length 85;
Best Local Similarity 100.0%; Pred. No. 6.9e-40;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFDQHRALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSSKMKLFSFTPAWN 60
DB 1 GLHFDQHRALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSSKMKLFSFTPAWN 60
QY 61 WTCKDLLLQAL 71
DB 61 WTCKDLLLQAL 71

RESULT 5
US-09-931-071-7
; Sequence 7, Application US/09931071
; Patent No. US20020128219A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-335001
; CURRENT APPLICATION NUMBER: US/09/931,071
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/428,252
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-931-071-7

Query Match      100.0%; Score 378; DB 9; Length 90;
Best Local Similarity 100.0%; Pred. No. 7.4e-40;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFDQHRALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSSKMKLFSFTPAWN 60
DB 6 GLHFDQHRALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSSKMKLFSFTPAWN 65
QY 61 WTCKDLLLQAL 71
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Db 61 WTCKDLLLQAL 71

RESULT 4
US-10-756-097-8
; Sequence 8, Application US/10756097
; Publication No. US20040127685A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND
; FILE REFERENCE: 07334-330001
; CURRENT APPLICATION NUMBER: US/10/756,097
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: US/09/841,879B
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 09/728,721
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/340,620
; PRIOR FILING DATE: 1999-06-28
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-756-097-8

Query Match      100.0%; Score 378; DB 16; Length 85;
Best Local Similarity 100.0%; Pred. No. 6.9e-40;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFDQHRALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSSKMKLFSFTPAWN 60
DB 1 GLHFDQHRALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSSKMKLFSFTPAWN 60
QY 61 WTCKDLLLQAL 71
DB 61 WTCKDLLLQAL 71

RESULT 5
US-09-931-071-7
; Sequence 7, Application US/09931071
; Patent No. US20020128219A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-335001
; CURRENT APPLICATION NUMBER: US/09/931,071
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/428,252
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-931-071-7

Query Match      100.0%; Score 378; DB 9; Length 90;
Best Local Similarity 100.0%; Pred. No. 7.4e-40;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFDQHRALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSSKMKLFSFTPAWN 60
DB 6 GLHFDQHRALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSSKMKLFSFTPAWN 65
QY 61 WTCKDLLLQAL 71
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Db 66 WTCKDLLLQAL 76
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RESULT 6

US-09-728-721-49

; Sequence 49, Application US/09728721

; Patent No. US20020061845A1

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE

; FILE REFERENCE: 07334-124001

; CURRENT APPLICATION NUMBER: US/09/728,721

; CURRENT FILING DATE: 2000-12-01

; PRIOR APPLICATION NUMBER: 09/340,620

; PRIOR FILING DATE: 1999-06-28

; PRIOR APPLICATION NUMBER: US 09/207,359

; PRIOR FILING DATE: 1998-12-08

; PRIOR APPLICATION NUMBER: US 09/099,041

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: US 09/019,942

; PRIOR FILING DATE: 1998-02-06

; NUMBER OF SEQ ID NOS: 71

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 49

; LENGTH: 195

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-728-721-49

Query Match 100.0%; Score 378; DB 9; Length 195;

Best Local Similarity 100.0%; Pred. No. 1.8e-39;

Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 60

Db 111 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 170

QY 61 WTCKDLLLQAL 71

|||||

Db 171 WTCKDLLLQAL 181

RESULT 7

US-09-996-617-8

; Sequence 8, Application US/09996617

; Patent No. US20020128198A1

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

; FILE REFERENCE: 07334-340001

; CURRENT APPLICATION NUMBER: US/09/996,617

; CURRENT FILING DATE: 2001-11-27

; PRIOR APPLICATION NUMBER: 09/931,071

; PRIOR FILING DATE: 2001-08-15

; PRIOR APPLICATION NUMBER: 09/428,252

; PRIOR FILING DATE: 1999-10-27

; PRIOR APPLICATION NUMBER: 09/340,620

; PRIOR FILING DATE: 1999-06-28

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 8

; LENGTH: 195

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-996-617-8

Query Match 100.0%; Score 378; DB 9; Length 195;

Best Local Similarity 100.0%; Pred. No. 1.8e-39;

Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 60

Db 111 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 170

Db 111 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 170
QY 61 WTCKDLLLQAL 71
|||||
Db 171 WTCKDLLLQAL 181

RESULT 8

US-09-841-879B-5

; Sequence 5, Application US/09841879B

; Patent No. US20020142979A1

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE

; FILE REFERENCE: 07334-330001

; CURRENT APPLICATION NUMBER: US/09/841,879B

; CURRENT FILING DATE: 2001-04-24

; PRIOR APPLICATION NUMBER: US 09/728,721

; PRIOR FILING DATE: 2000-12-01

; PRIOR APPLICATION NUMBER: US 09/340,620

; PRIOR FILING DATE: 1999-06-28

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 195

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-841-879B-5

Query Match 100.0%; Score 378; DB 9; Length 195;

Best Local Similarity 100.0%; Pred. No. 1.8e-39;

Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 60

Db 111 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 170

QY 61 WTCKDLLLQAL 71

|||||

Db 171 WTCKDLLLQAL 181

RESULT 9

US-10-446-046-4

; Sequence 4, Application US/10446046

; Publication No. US20030224438A1

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR

; FILE REFERENCE: MPI02-081P1RM

; CURRENT APPLICATION NUMBER: US/10/446,046

; CURRENT FILING DATE: 2003-05-23

; PRIOR APPLICATION NUMBER: 60/383487

; PRIOR FILING DATE: 2002-05-24

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 195

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-446-046-4

Query Match 100.0%; Score 378; DB 12; Length 195;

Best Local Similarity 100.0%; Pred. No. 1.8e-39;

Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 60

Db 111 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 170

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QY      61 WTCKDLLLQAL 71
Db      171 WTCKDLLLQAL 181

RESULT 10
US-10-295-981-49
; Sequence 49, Application US/10295981
; Publication No. US2003012055A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/10/295,981
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-981-49

Query Match      100.0%; Score 378; DB 14; Length 195;
Best Local Similarity 100.0%; Pred. No. 1.8e-39;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLHFIDQHRAALIAIARVTNVVWLLDALYKGLVTDQYQAVRAEPTNPSPKMKLFSTFPWN 60
Db      111 GLHFIDQHRAALIAIARVTNVVWLLDALYKGLVTDQYQAVRAEPTNPSPKMKLFSTFPWN 170

QY      61 WTCKDLLLQAL 71
Db      171 WTCKDLLLQAL 181

RESULT 11
US-10-240-145-55
; Sequence 55, Application US/10240145
; Publication No. US2003023583A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-048
; CURRENT APPLICATION NUMBER: US/10/240,145
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/668,680
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/695,618
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 09/728,711
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: NOT YET ASSIGNED
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: Custom
; SEQ ID NO 55
; LENGTH: 195
; TYPE: PRT
US-10-240-145-55
```

```
; ORGANISM: Homo sapiens
US-10-240-145-55

Query Match      100.0%; Score 378; DB 15; Length 195;
Best Local Similarity 100.0%; Pred. No. 1.8e-39;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLHFIDQHRAALIAIARVTNVVWLLDALYKGLVTDQYQAVRAEPTNPSPKMKLFSTFPWN 60
Db      111 GLHFIDQHRAALIAIARVTNVVWLLDALYKGLVTDQYQAVRAEPTNPSPKMKLFSTFPWN 170

QY      61 WTCKDLLLQAL 71
Db      171 WTCKDLLLQAL 181

RESULT 12
US-10-131-410-84
; Sequence 84, Application US/10131410
; Publication No. US20030235915A1
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM TISSUE OF BREAST
; TITLE OF INVENTION: TUMORS
; FILE REFERENCE: SCH-1763
; CURRENT APPLICATION NUMBER: US/10/131,410
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 09/646,673
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: PCT/DE99/00908
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-410-84

Query Match      100.0%; Score 378; DB 15; Length 195;
Best Local Similarity 100.0%; Pred. No. 1.8e-39;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLHFIDQHRAALIAIARVTNVVWLLDALYKGLVTDQYQAVRAEPTNPSPKMKLFSTFPWN 60
Db      111 GLHFIDQHRAALIAIARVTNVVWLLDALYKGLVTDQYQAVRAEPTNPSPKMKLFSTFPWN 170

QY      61 WTCKDLLLQAL 71
Db      171 WTCKDLLLQAL 181

RESULT 13
US-10-756-097-5
; Sequence 5, Application US/10756097
; Publication No. US20040127685A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND
; FILE REFERENCE: 07334-330001
; CURRENT APPLICATION NUMBER: US/10/756,097
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: US/09/841,879B
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 09/728,721
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/340,620
```

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; PRIOR FILING DATE: 1999-06-28
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-756-097-5

Query Match      100.0%; Score 378; DB 16; Length 195;
Best Local Similarity 100.0%; Pred. No. 1.8e-39;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 60
Db 111 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 170
Qy 61 WTCKDLLLQAL 71
Db 171 WTCKDLLLQAL 181

RESULT 14
US-10-106-698-5421
; Sequence 5421, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: Patentin ver. 3.0
; SEQ ID NO 5421
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-698-5421

Query Match      100.0%; Score 378; DB 14; Length 205;
Best Local Similarity 100.0%; Pred. No. 1.9e-39;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 60
Db 121 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 180
Qy 61 WTCKDLLLQAL 71
Db 181 WTCKDLLLQAL 191

RESULT 15
US-09-841-879B-15
; Sequence 15, Application US/09841879B
; Patent No. US20020142979A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-330001
; CURRENT APPLICATION NUMBER: US/09/841,879B
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 09/728,721
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/340,620
; PRIOR FILING DATE: 1999-06-28
```

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; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 2, 5, 18, 20, 21, 29, 34, 45-47, 56, 61, 67, 72, 74-75, 84
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-841-879B-15

Query Match      71.2%; Score 269; DB 9; Length 85;
Best Local Similarity 76.1%; Pred. No. 4.1e-26;
Matches 54; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Qy 1 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 60
Db 1 GXHFYDQHRAALIAIARVTXXXVLDALYGVLTDEQYQAVRAETTTXXXKXKRLFSFXPSMN 60
Qy 61 WTCKDLLLQAL 71
Db 61 XTCKDXLLQAL 71
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Search completed: July 28, 2004, 09:04:14
Job time : 34.6446 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2004, 08:50:22 ; Search time 10.2651 Seconds
(without alignments)
665.325 Million cell updates/sec

Title: US-09-996-617-8_COPY_111_181
Perfect score: 378
Sequence: 1 GLHFIDQHRALIAIARTVNE.....LFSFTPAWNTCKDLLLQAL 71

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78: *
1: piri: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	216	57.1	1192	2 T17255	hypothetical prote
2	69.5	18.4	221	2 S70009	glutamate/proline-
3	68	18.0	545	2 A87136	hypothetical prote
4	64.5	17.1	605	2 T04197	hypothetical prote
5	64	16.9	304	2 G81417	cytochrome-c perox
6	62.5	16.5	211	2 S57340	YggA protein homol
7	62	16.4	779	2 A82402	alpha-glucosidase
8	61.5	16.3	306	2 T21132	hypothetical prote
9	61.5	16.3	346	2 A48470	translation elonga
10	61.5	16.3	1193	2 T21133	hypothetical prote
11	61	16.1	277	2 F83616	hypothetical prote
12	61	16.1	338	2 AF0294	probable lipote-p
13	61	16.1	345	2 T17608	probable GPMannos
14	60.5	16.0	464	2 H82011	probable outer mem
15	60.5	16.0	724	2 C71274	hypothetical prote
16	60.5	16.0	877	2 JN0772	glucan endo-1,3-be
17	60	15.9	332	2 C83295	conserved hypothet
18	60	15.9	773	2 T39513	hypothetical prote
19	59.5	15.7	249	2 A35363	beta-lactamase (EC
20	59.5	15.7	290	2 I58425	arylamine N-acetyl
21	59	15.6	286	2 B82201	spermidine/puresc
22	59	15.6	371	2 S68072	major outer membra
23	59	15.6	381	2 B88437	protein R0735.3 [i
24	59	15.6	529	2 S43599	Snf5 homolog R07E5
25	59	15.6	537	2 S62749	A-alpha X protein
26	59	15.6	542	2 D70873	probable ABC trans
27	59	15.6	681	2 E70942	hypothetical prote
28	59	15.6	1021	2 S09111	hypothetical prote
29	59	15.6	1023	2 G96509	protein F27F5.21 [

30 58.5 15.5 290 2 B61267
31 58.5 15.5 368 2 T04861
32 58.5 15.5 443 2 C75143
33 58.5 15.5 498 2 AD0978
34 58.5 15.5 554 2 S46346
35 58.5 15.5 700 2 B82788
36 58 15.3 192 2 A12271
37 58 15.3 371 2 S68069
38 57.5 15.2 156 2 AG3373
39 57.5 15.2 280 2 F70943
40 57.5 15.2 290 2 I67485
41 57.5 15.2 350 2 B39364
42 57.5 15.2 380 2 T29544
43 57.5 15.2 446 2 S16308
44 57.5 15.2 682 2 J00420
45 57 15.1 233 2 S62063

ALIGNMENTS

RESULT 1

T17255
hypothetical protein DKFp586O1822.1 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T17255
R:Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A:Reference number: Z18722
A:Accession: T17255
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1192 <KOE>
A:Cross-references: EMBL:AL117470
A:Experimental source: adult uterus; clone DKFp586O1822
C:Genetics:
A>Note: DKFp586O1822.1

Query Match 57.1%; Score 216; DB 2; Length 1192;
Best Local Similarity 61.4%; Pred. No. 6.1e-17;
Matches 43; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 2 LHFIDQHRALIAIARTVNTVEWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWNT 61
DB 1098 LHFVDQYREQLIARTVTSVEVLDLHGQVLSQEQYERVIAENTRPSKMKLFSQSQWDR 1157
QY 62 TCKDLLLQAL 71
DB 1158 KCKDGLYQAL 1167

RESULT 2

S70009
glutamate/proline-rich protein (clone 53.1.1.1) - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 06-Dec-1995 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C:Accession: S70009
R:Geertman, R.; McMahon, A.; Sabban, E.L.
Biochim. Biophys. Acta 1306, 147-152, 1996
A:Title: Cloning and characterization of cDNAs for novel proteins with glutamic acid-pr
A:Reference number: S70009; MUID:96221285; PMID:8634331
A:Accession: S70009
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-221 <GEE>
A:Cross-references: EMBL:U40627; NID:g1184693; PIDN:AAB05667.1; PID:g1184694

Query Match 18.4%; Score 69.5; DB 2; Length 221;
Best Local Similarity 26.8%; Pred. No. 1.3;
Matches 22; Conservative 12; Mismatches 23; Indels 25; Gaps 3;

QY 5 IDQHRALIAIARV-TNVEWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFT----- 56

R;Kaneke, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AE2402
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-779 <WIL>
A;Cross-references: GB:BA000019; PIDN:BAE76472.1; PID:G17133910; GSPDB:GNO0179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: air4773

Query Match 16.4%; Score 62; DB 2; Length 779;
Best Local Similarity 35.7%; Pred. No. 41;
Matches 15; Conservative 6; Mismatches 13; Indels 8; Gaps 2;

QY 6 DQH-----RAALIARTNV--FWLLDALYGVLTDEQYQAV 39
| | | | | : : : : : | | | | | : : : : :
DQ H A A L I A R T N V - - F W L L D A L Y G V L T D E Q Y Q A V

DB 141 DEHYFGERTGLDQIATIRTNWACDALDYDLTDMYQAI 182
| | | | | : : : : : | | | | | : : : : :
D E H Y F G E R T G L D Q I A T I R T N W A C D A L D Y D L T D M Y Q A I

RESULT 8
T21132
hypothetical protein F20B10.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21132
R;Percy, C.
submitted to the EMBL Data Library, February 1996
A;Reference number: Z19380
A;Accession: T21132
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-306 <WIL>
A;Cross-references: EMBL:Z69636; PIDN:CAA93464.1; GSPDB:GNO0022; CESP:F20B10.2
A;Experimental source: Clone F20B10
C;Genetics:
A;Gene: CESP:F20B10.2
A;Map position: 4
A;Introns: 18/1; 74/3; 135/1; 222/3; 258/3; 279/1

Query Match 16.3%; Score 61.5; DB 2; Length 306;
Best Local Similarity 34.0%; Pred. No. 17;
Matches 17; Conservative 10; Mismatches 20; Indels 3; Gaps 2;

QY 13 IARVT--NVEWLLDALYGV-LTDEQYQAVRAEPTNPSKMKLFSTPAW 59
: | | | : : : : : | | | : : : : :
I A R V T - - N V E W L L D A L Y G V - L T D E Q Y Q A V R A E P T N P S K M K L F S T P A W

DB 37 LKRVRLSVSGHISAVHKVYSISDDDFQLVRLSNGNPLVLYSLNTSPW 86
: | | | : : : : : | | | : : : : :
L K R V R L S V S G H I S A V H K V Y S I S D D F Q L V R L S N G N P L V L Y S L N T S P W

RESULT 9
A48470
translation elongation factor eEF-1 alpha chain - Eimeria bovis (fragment)
C;Species: Eimeria bovis
C;Date: 01-Dec-1993 #sequence_revision 15-Oct-1994 #text_change 12-Apr-1995
C;Accession: A48470
R;Abrahamsen, M.S.; Clark, T.G.; Mascolo, P.; Speer, C.A.; White, M.W.
Mol. Biochem. Parasitol. 57, 1-14, 1993
A;Title: Developmental gene expression in Eimeria bovis.
A;Reference number: A48470; MUID:93149194; PMID:8426605
A;Accession: A48470
A;Molecule type: mRNA
A;Residues: 1-346 <ABR>
A;Experimental source: merozoites
A;Note: sequence extracted from NCBI backbone (NCBI:123619, NCBI:123622)
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog
C;Keywords: GTP binding; protein biosynthesis

Query Match 16.3%; Score 61.5; DB 2; Length 346;
Best Local Similarity 21.7%; Pred. No. 19;
Matches 15; Conservative 13; Mismatches 34; Indels 7; Gaps 1;

QY 13 IARVT--NVEWLLDALYGV-LTDEQYQAVRAEPTNPSKMKLFSTPAW 59
: | | | : : : : : | | | : : : : :
I A R V T - - N V E W L L D A L Y G V - L T D E Q Y Q A V R A E P T N P S K M K L F S T P A W

DB 37 LKRVRLSVSGHISAVHKVYSISDDDFQLVRLSNGNPLVLYSLNTSPW 86
: | | | : : : : : | | | : : : : :
L K R V R L S V S G H I S A V H K V Y S I S D D F Q L V R L S N G N P L V L Y S L N T S P W

RESULT 9
A48470
translation elongation factor eEF-1 alpha chain - Eimeria bovis (fragment)
C;Species: Eimeria bovis
C;Date: 01-Dec-1993 #sequence_revision 15-Oct-1994 #text_change 12-Apr-1995
C;Accession: A48470
R;Abrahamsen, M.S.; Clark, T.G.; Mascolo, P.; Speer, C.A.; White, M.W.
Mol. Biochem. Parasitol. 57, 1-14, 1993
A;Title: Developmental gene expression in Eimeria bovis.
A;Reference number: A48470; MUID:93149194; PMID:8426605
A;Accession: A48470
A;Molecule type: mRNA
A;Residues: 1-346 <ABR>
A;Experimental source: merozoites
A;Note: sequence extracted from NCBI backbone (NCBI:123619, NCBI:123622)
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog
C;Keywords: GTP binding; protein biosynthesis

Query Match 16.3%; Score 61.5; DB 2; Length 346;
Best Local Similarity 21.7%; Pred. No. 19;
Matches 15; Conservative 13; Mismatches 34; Indels 7; Gaps 1;

QY 13 IARVT--NVEWLLDALYGV-LTDEQYQAVRAEPTNPSKMKLFSTPAW 59
: | | | : : : : : | | | : : : : :
I A R V T - - N V E W L L D A L Y G V - L T D E Q Y Q A V R A E P T N P S K M K L F S T P A W

DB 37 LKRVRLSVSGHISAVHKVYSISDDDFQLVRLSNGNPLVLYSLNTSPW 86
: | | | : : : : : | | | : : : : :
L K R V R L S V S G H I S A V H K V Y S I S D D F Q L V R L S N G N P L V L Y S L N T S P W

RESULT 9
A48470
translation elongation factor eEF-1 alpha chain - Eimeria bovis (fragment)
C;Species: Eimeria bovis
C;Date: 01-Dec-1993 #sequence_revision 15-Oct-1994 #text_change 12-Apr-1995
C;Accession: A48470
R;Abrahamsen, M.S.; Clark, T.G.; Mascolo, P.; Speer, C.A.; White, M.W.
Mol. Biochem. Parasitol. 57, 1-14, 1993
A;Title: Developmental gene expression in Eimeria bovis.
A;Reference number: A48470; MUID:93149194; PMID:8426605
A;Accession: A48470
A;Molecule type: mRNA
A;Residues: 1-346 <ABR>
A;Experimental source: merozoites
A;Note: sequence extracted from NCBI backbone (NCBI:123619, NCBI:123622)
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog
C;Keywords: GTP binding; protein biosynthesis

Query Match 16.3%; Score 61.5; DB 2; Length 346;
Best Local Similarity 21.7%; Pred. No. 19;
Matches 15; Conservative 13; Mismatches 34; Indels 7; Gaps 1;

QY 13 IARVT--NVEWLLDALYGV-LTDEQYQAVRAEPTNPSKMKLFSTPAW 59
: | | | : : : : : | | | : : : : :
I A R V T - - N V E W L L D A L Y G V - L T D E Q Y Q A V R A E P T N P S K M K L F S T P A W

DB 37 LKRVRLSVSGHISAVHKVYSISDDDFQLVRLSNGNPLVLYSLNTSPW 86
: | | | : : : : : | | | : : : : :
L K R V R L S V S G H I S A V H K V Y S I S D D F Q L V R L S N G N P L V L Y S L N T S P W

QY 5 IDQRAALIARVTVNVEWLLDALYGVLTDE-----QYQAVRAEPTNPSKMKLFSTFP 57
: | | | : : : : : | | | : : : : :
I D Q R A A L I A R V T V N V E W L L D A L Y G V L T D E - - - - - Q Y Q A V R A E P T N P S K M K L F S T F P

DB 246 VDCHTAHTACKFAVLKELDRSGKALDDPKFKTKTGDAAIKMEPSKMCVSPFIEYFP 305
: | | | : : : : : | | | : : : : :
V D C H T A H T A C K F A V L K E L D R S G K A L D D P K F K T K T G D A A I K M E P S K M C V S P F I E Y F P

QY 58 AWWTKDGL 66
: | | : : : : :
A W W T K D G L

DB 306 LGRFVRDM 314
: | | : : : : :
L G R F V R D M

RESULT 10
T21133
hypothetical protein F20B10.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21133
R;Percy, C.
submitted to the EMBL Data Library, February 1996
A;Reference number: Z19380
A;Accession: T21133
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1193 <WIL>
A;Cross-references: EMBL:Z69636; PIDN:CAA93465.1; GSPDB:GNO0022; CESP:F20B10.1
A;Experimental source: Clone F20B10
C;Genetics:
A;Gene: CESP:F20B10.1
A;Map position: 4
A;Introns: 18/1; 74/3; 135/1; 222/3; 258/3; 279/1; 496/1; 791/2; 867/1; 969/1; 1

Query Match 16.3%; Score 61.5; DB 2; Length 1193;
Best Local Similarity 34.0%; Pred. No. 76;
Matches 17; Conservative 10; Mismatches 20; Indels 3; Gaps 2;

QY 13 IARVT--NVEWLLDALYGV-LTDEQYQAVRAEPTNPSKMKLFSTPAW 59
: | | | : : : : : | | | : : : : :
I A R V T - - N V E W L L D A L Y G V - L T D E Q Y Q A V R A E P T N P S K M K L F S T P A W

DB 37 LKRVRLSVSGHISAVHKVYSISDDDFQLVRLSNGNPLVLYSLNTSPW 86
: | | | : : : : : | | | : : : : :
L K R V R L S V S G H I S A V H K V Y S I S D D F Q L V R L S N G N P L V L Y S L N T S P W

RESULT 11
F83616
hypothetical protein PA0234 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83616
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83616
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-277 <STO>
A;Cross-references: GB:AE004461; GB:AE004091; NID:G9946066; PIDN:AAG03623.1; GSPDB:GNO0
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA0234

Query Match 16.1%; Score 61; DB 2; Length 277;
Best Local Similarity 32.8%; Pred. No. 17;
Matches 20; Conservative 11; Mismatches 12; Indels 18; Gaps 4;

QY 7 QHRAALIARV-----TNVEWLLDAL---YGVLTDEQYQAVRAEPTNPSKM-RKLFSTFP 57
: | | | | | : : : : : | | | : : : : :
Q H R A A L I A R V - - - - - T N V E W L L D A L - - - Y G V L T D E Q Y Q A V R A E P T N P S K M - R K L F S T F P

DB 6 QQAALIALVGAGESMALEWNSVGFYGOQFTN-----PNNPKAKRIYSPTH 56
: | | | | | : : : : : | | | : : : : :
Q Q A A L I A L V G A G E S M A L E W N S V G F Y G O Q F T N - - - - - P N N P K A K R I Y S P T H

QY 58 A 58
57 A 57

RESULT 12

AF0294
C: probable lipopate-protein ligase A lplA [imported] - Yersinia pestis (strain CO92)
C: Species: Yersinia pestis
C: Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
A: Accession: AF0294
R: Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell, Nature 413, 523-527, 2001
A: Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A: Reference number: AB0001; MUID:21470413; PMID:11586360
A: Accession: AF0294
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-338 <KUR>
A: Cross-references: GB:AL590842; PIDN:CA091218.1; PID:gl5980407; GSPDB:GN00175
C: Genetics:
A: Gene: lplA
C: Superfamily: lipopate-protein ligase

Query Match 16.1%; Score 61; DB 2; Length 338;
Best Local Similarity 32.3%; Pred. No. 21;
Matches 21; Conservative 8; Mismatches 16; Indels 20; Gaps 4;
QY 14 ARVTNVEWLLDAL-YGKVLTDQYQAVRAEPTNPSKMKLFSFT----- 56
DB 183 SRVNLVELFGIDHGKIRTAIEQAFYAYDEQ---VSAEIVSQSLPNLPFGTEQFAKQ 239
QY 57 PAWNW 61
DB 240 SSNEW 244

RESULT 13

Ti7608
C: probable GDPmannose 4,6-dehydratase (EC 4.2.1.47) - Chlorella virus PBCV-1
N: Alternate names: GDP-D-mannose dehydratase
C: Species: Chlorella virus PBCV-1
C: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
A: Accession: Ti7608
R: Graves, M.V.; Van Etten, J.L.
A: Submitted to the EMBL Data Library, May 1999
A: Reference number: 218806
A: Accession: Ti7608
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-345 <GRA>
A: Cross-references: EMBL:U42580; NID:94028896; PIDN:AAC96486.1
A: Experimental source: specific host Chlorella strain NC64A
C: Genetics:
A: Note: AllOR
C: Superfamily: GDP-D-mannose dehydratase
C: Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 16.1%; Score 61; DB 2; Length 345;
Best Local Similarity 28.6%; Pred. No. 22;
Matches 22; Conservative 9; Mismatches 22; Indels 24; Gaps 3;
QY 8 HRAALIAIV--TNVWLLDA-----LYGKVLTDQYQAVRAEPTNPSK 48
DB 91 HQAEVTANVDALGVLLRLDAVRIAGLNSRICQASTSELYGKVGQEIPTQRTFFPRSPYG 150
QY 49 MKLPSFTPAWNWTKD 65
DB 151 VAKLYAY-----WICKN 162

RESULT 14

H82011
C: probable outer membrane protein NMA0178 [imported] - Neisseria meningitidis (strain Z249)
C: Species: Neisseria meningitidis
C: Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001

C: Accession: H82011
R: Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, J.; Holtroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A: Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A: Reference number: A81775; MUID:20222556; PMID:10761919
A: Accession: H82011
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-464 <PAR>
A: Cross-references: GB:AL162752; GB:AL157959; NID:97378778; PIDN:CA83493.1; PID:9737895
A: Experimental source: serogroup A, strain Z2491
C: Genetics:
A: Gene: NMA0178

Query Match 16.0%; Score 60.5; DB 2; Length 464;
Best Local Similarity 25.7%; Pred. No. 35;
Matches 18; Conservative 13; Mismatches 22; Indels 17; Gaps 2;

QY 10 AALIAIVTNVEWLLDALYGKVLTDQYQAVRAEPTNPSKMKL-----PSF 55
DB 173 AGIIAHTSAELRYKVDWIM---EKALKETPPNPTKAAQIKADGHADVKGSDWNGFY 229
QY 56 TPAWNWTKD 65
DB 230 QLAWWWDIND 239

RESULT 15

C71274
C: hypothetical protein TP0851 - syphilis spirochete
C: Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C: Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 24-Nov-1999
C: Accession: C71274
R: Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinn, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDermott, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
A: Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A: Reference number: A71250; MUID:98332770; PMID:9665876
A: Accession: C71274
A: Status: preliminary; nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA
A: Residues: 1-724 <COL>
A: Cross-references: GB:AE001255; GB:AE000520; NID:93323156; PIDN:AAC65821.1; PID:9332318
A: Experimental source: strain Nichols
C: Genetics:
A: Gene: TP0851
C: Superfamily: syphilis spirochete hypothetical protein TP0851

Query Match 16.0%; Score 60.5; DB 2; Length 724;
Best Local Similarity 26.9%; Pred. No. 57;
Matches 21; Conservative 17; Mismatches 27; Indels 13; Gaps 5;

QY 3 HFIDQHRAALIAIVTNVEWLLDALYGK-VLTDEYQAVR--AEPTNPSKMKLPSF---- 55
DB 132 YIIGHN--VILSRIDELCTTHAKFGAGIIKDGEQEAVRITIDPLNETGGRKIFPFVGM 189
QY 56 -TPAWNWTG---KDLILLQ 69
DB 190 AADAFELWACHRDPTLLMQ 207

Search completed: July 28, 2004, 08:55:21
Job time : 12.2651 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2004, 08:46:37 ; Search time 6.84337 seconds
(without alignments)
540.228 Million cell updates/sec

Title: US-09-996-617-8_COPY_111_181

Perfect score: 378

Sequence: 1 GLHFIDQHRALFARVTVSE.....LFSFTPAWNWCKDLLLQAL 71

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	378	100.0	195	1	Q9ulz3 homo sapien
2	264	69.8	193	1	Q9epb4 mus musculu
3	216	57.1	1473	1	Q9c000 homo sapien
4	106	28.0	203	1	Q919n6 brachydanio
5	69.5	18.4	219	1	Q60936 homo sapien
6	69.5	18.4	220	1	Q9dix0 mus musculu
7	69.5	18.4	221	1	Q62881 rattus norv
8	68.5	18.1	431	1	Q9y292 homo sapien
9	67.5	17.9	539	1	Q58801 mus musculu
10	66.5	17.6	611	1	Q90860 gallus gall
11	65	17.2	598	1	Q8k301 mus musculu
12	64.5	17.1	953	1	Q9y239 homo sapien
13	62.5	16.5	225	1	P52047 aeromonas h
14	62.5	16.5	540	1	Q43353 h receptor-
15	62	16.4	598	1	Q99b00 rattus norv
16	61.5	16.3	346	1	Q07051 eimeria bov
17	60.5	16.0	724	1	Q83823 treponema p
18	60	15.9	259	1	Q96pb8 homo sapien
19	60	15.9	259	1	Q8vch9 mus musculu
20	60	15.9	332	1	Q91048 pseudomonas
21	60	15.9	494	1	P79784 gallus gall
22	59.5	15.7	249	1	P25910 bacteroides
23	59.5	15.7	290	1	P50398 rattus norv
24	59.5	15.7	347	1	Q8r059 mus musculu
25	59	15.6	290	1	Q8k8u9 streptococc
26	59	15.6	371	1	P46027 haemophilus
27	59	15.6	1021	1	P16425 drosophila
28	58.5	15.5	290	1	P50295 mus musculu
29	58.5	15.5	612	1	Q62210 mus musculu
30	58.5	15.5	953	1	Q8bb0 mus musculu
31	58	15.3	117	1	Q32723 bacillus ep
32	57.5	15.2	290	1	P50297 rattus norv
33	57.5	15.2	350	1	P27545 mus musculu

34 57.5 15.2 446 1 ERIA_STYLE
35 57.5 15.2 682 1 E13B_BACCI
36 57.5 15.2 721 1 MASZ_RHILO
37 57 15.1 233 1 VATE_YEAST
38 57 15.1 375 1 YBFF_VIBCH
39 57 15.1 508 1 MM19_HUMAN
40 56.5 14.9 290 1 ARV1_HUMAN
41 56.5 14.9 347 1 GALE_RAT
42 56.5 14.9 463 1 EF11_XENLA
43 56.5 14.9 609 1 YL15_MYCTU
44 56.5 14.9 621 1 FX21_HUMAN
45 56.5 14.9 1634 1 PK3B_HUMAN

ALIGNMENTS

RESULT 1
ASC_HUMAN
ID ASC_HUMAN STANDARD; PRT; 195 AA.
AC Q9ULZ3; Q96D12; Q9BS25; Q9HBD0; Q9NXJ8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Apoptosis-associated speck-like protein containing a CARD (hASC)
DE (PYCARD) (Target of methylation-induced silencing 1) (Caspase
DE recruitment domain protein 5).
GN ASC OR TMS1 OR CARD5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20036508; PubMed=10567338;
RA Masumoto J., Iatiguchi S., Ayukawa K., Sarvotham H., Kishino T.,
RA Nukawa N., Hidaka E., Katsuyama T., Higuchi T., Sagara J.;
RT "ASC, a novel 22-kDa protein, aggregates during apoptosis of human
RT promyelocytic leukemia HL-60 cells.";
RL J. Biol. Chem. 274:33835-33838(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=20552139; PubMed=11103776;
RA Conway K.E., McConnell B.B., Bowring C.E., Donald C.D., Warren S.T.,
RA Vertino P.M.;
RT "TMS1, a novel proapoptotic caspase recruitment domain protein, is a
RT target of methylation-induced gene silencing in human breast
RT cancers.";
RL Cancer Res. 60:6236-6242(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Martinon F., Hofmann K., Tschopp J.;
RT "PYCARD a PYD and CARD containing molecule.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Bertin J.;
RT "CARD5 protein is a CARD/PYRIN family member that is involved in
RT apoptosis signal transduction.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
RA Suzuki Y., Ohtsuka M., Nishi T., Shibahara T., Tanaka T.,
RA Nakamura Y., Isegaki T., Sugano S.;
RT "NEDD human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
RT TISSUE=Lymph, and Pancreas;

RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP FUNCTION, AND SUBCELLULAR LOCATION.
RX MEDLINE=20552140; PubMed=1103777;
RA McConnell B.B., Vertino P.M.,
RT "Activation of a caspase-9-mediated apoptotic pathway by subcellular
RT redistribution of the novel caspase recruitment domain protein TMS1.";
RL Cancer Res. 60:6243-6247(2000).
CC -!- FUNCTION: Promotes caspase-mediated apoptosis. This proapoptotic
CC activity is mediated predominantly through the activation of
CC caspase 9.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Upstream of caspase activation,
CC a redistribution from the cytoplasm to the aggregates occurs.
CC These appeared as hollow, perinuclear spherical, ball-like
CC structures.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q9ULZ3-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9ULZ3-2; Sequence=VSP_004119;
CC Name=3;
CC IsoId=Q9ULZ3-3; Sequence=VSP_004118;
CC Note-No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Widely expressed at low levels. Detected in
CC peripheral blood leukocytes, lung, small intestine, spleen,
CC thymus, colon and at lower levels in placenta, liver and kidney.
CC Very low expression in skeletal muscle, heart and brain. Detected
CC in the leukemia cell lines HL-60 and U937, but not in Jurkat T-
CC cell lymphoma and Daudi Burkitt's lymphoma. Detected in the
CC melanoma cell line WM35, but not in WM793. Not detected in HeLa
CC cervical carcinoma cells and Molt 4 lymphocytic leukemia cells.
CC -!- MISCELLANEOUS: In breast tumorigenesis, methylation-mediated
CC silencing may affect genes and proteins that act as positive
CC mediators of cell death.
CC -!- SIMILARITY: Contains 1 DAPIN domain.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC -!- CAUTION: Ref.5 sequence differs from that shown due to a
CC frameshift in position 4.
CC -----
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CC or send an email to licences@isb.sib.ch).
CC -----
DR EMBL; AB023416; BAA87339.2; -;
DR EMBL; AF184072; AAG01187.1; -;
DR EMBL; AF184073; AAG01188.1; -;
DR EMBL; AF255794; AAF9965.1; -;
DR EMBL; AF310103; AAG30286.1; -;

DR EMBL; AF384665; AAK63850.1; -;
DR EMBL; AK000211; BAA91012.1; ALT_FRAME.
DR EMBL; BC004470; AAH04470.1; -;
DR EMBL; BC013569; AAH13569.1; ALT_INIT.
DR MIM; 606838; -;
DR GO; GO:0006917; P:induction of apoptosis; TAS.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR004020; PAAD DAPIN_dom.
DR Pfam; PF02758; PAAD DAPIN; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS50824; DAPIN; 1.
KW Apoptosis; Anti-oncogene; Alternative splicing.
FT DOMAIN 1 91
FT DAPIN.
FT CARD.
FT VARSPLIC 26 85
FT Missing (in isoform 3).
FT VARSPLIC 93 111
FT Missing (in isoform 2).
FT FTID=VSP_004119.
FT FTID=VSP_004118.
SQ SEQUENCE 195 AA; 21627 MW; 455987286586F46A CRC64;
Query Match 100.0%; Score 378; DB 1; Length 195;
Best Local Similarity 100.0%; Pred. No. 3.3e-37;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLHFDQHRALITARTVNVEMLLDALYKGLTDEQYQAVRAEPTNPVKRKLFSFTPAWN 60
DB 111 GLHFDQHRALITARTVNVEMLLDALYKGLTDEQYQAVRAEPTNPVKRKLFSFTPAWN 170
QY 61 WTCKDLILQAL 71
DB 171 WTCKDLILQAL 181
RESULT 2
ASC MOUSE
ID ASC MOUSE STANDARD; PRT; 193 AA.
AC Q9EPB4; Q9D2W9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2003 (Rel. 42, Last annotation update)
DE Apoptosis-associated speck-like protein containing a CARD (mASC)
DE (PYCARD).
GN ASC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Thymus;
RX MEDLINE=20580347; PubMed=11139337;
RA Masumoto J., Taniguchi S., Nakayama K., Ayukawa K., Sagara J.;
RT "Murine ortholog of ASC, a CARD-containing protein, self-associates
RT and exhibits restricted distribution in developing mouse embryos.";
RL Exp. Cell Res. 262:128-133(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Breast tumor;
RX Martinon F., Hofmann K., Tschopp J.;
RT "PyCARD a PYD and CARD containing molecule.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas; and Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawal J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Niehi K., Kiyosawa H., Kondo S., Yamakura I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glassi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barh G., Blake J., Boffelli D., Bojuna N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hune D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Hayashizaki Y., Hynes-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S., Hayashizaki Y.,

RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[4]

SEQUENCE FROM N.A.
RN MEDLINE=22388257; PubMed=12477932;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hoieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W., Vallalun D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Vining J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences".
RL Proc Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
CC -1- FUNCTION: Promotes caspase-mediated apoptosis. This proapoptotic activity is mediated predominantly through the activation of caspase 9 (by similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Upstream of caspase activation, a redistribution from the cytoplasm to the aggregates occurs. These appeared as hollow, perinuclear spherical, ball-like structures (by similarity).

CC -1- TISSUE SPECIFICITY: Expressed in small intestine, colon, thymus, spleen, brain, heart, skeletal muscle, kidney, lung and liver.

CC -1- DEVELOPMENTAL STAGE: Strongly expressed at E3.5 day in the telencephalon, thalamic areas of the diencephalon, heart and liver.

CC -1- SIMILARITY: Contains 1 DAPIN domain.
CC -1- SIMILARITY: Contains 1 CARD domain.

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CC ENBL; AB032249; BAB16609.1; -
CC ENBL; AF310104; AAG30287.1; -
CC ENBL; AKG09852; BAB26543.1; -
CC ENBL; AK07742; BAB25229.1; -
CC ENBL; AK018682; BAB31341.1; -
CC ENBL; BC008252; AAH08252.1; -
CC MGD; MGI:1931465; Asc.
CC GO; GO:0005829; Cytosol; IDA.
CC InterPro; IPR001315; CARD.
CC InterPro; IPR004020; PAAD DAPIN_dom.
CC Pfam; PF02758; PAAD DAPIN; 1.
CC PROSITE; PS50203; CARD; 1.
CC PROSITE; PS50824; DAPIN; 1.
CC Apoptosis; Anti-oncogene.
FT DOMAIN 1 DAPIN

[illegible]

RT for large proteins in vitro.;

RL DNA Res. 6:63-70(1999).

RN [6]

RP SEQUENCE OF 282-1473 FROM N.A. (ISOFORM 1).

RC TISSUE=Uterus;

RA Koehrer K., Beyer A., Mewes H.-W., Gassenhuber J., Wiemann S.;

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Able to form cytoplasmic structures termed death

CC effector filaments. Enhances APAF1 and cytochrome c-dependent

CC activation of pro-caspase-9 and consecutive apoptosis. Seems to

CC activate ATP.

CC -!- SUBUNIT: Interacts strongly with caspase 2, weakly with caspase 9

CC and with APAF1 in a cytochrome c-inducible way leading to the

CC formation of an apoptosome. This interaction may be ATP-dependent.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- ALTERNATIVE PRODUCTS:

CC Event-Alternative splicing; Named isoforms=4;

CC Name=1; Synonyms=NAC beta, DEFCAP-L;

CC IsoId=Q9C000-1; Sequence=Displayed;

CC Name=2; Synonyms=NAC alpha, DEFCAP-S;

CC IsoId=Q9C000-2; Sequence=VSP_004327;

CC Name=3; Synonyms=NAC gamma;

CC IsoId=Q9C000-3; Sequence=VSP_004326, VSP_004327;

CC Name=4; Synonyms=NAC delta; Sequence=VSP_004326;

CC IsoId=Q9C000-4; Sequence=VSP_004326;

CC -!- TISSUE SPECIFICITY: Widely expressed. Isoforms 1 and 2 are

CC expressed in peripheral blood leukocytes, chronic myelogenous

CC leukemia cell line K-562, followed by thymus, spleen and heart.

CC Also detected in lung, placenta, small intestine, colon, kidney,

CC liver and muscle.

CC -!- SIMILARITY: Contains 1 DAPIN domain.

CC -!- SIMILARITY: Contains 1 NACHT domain.

CC -!- SIMILARITY: Contains 1 CARD domain.

CC -!- SIMILARITY: Contains 7 leucine-rich (LRR) repeats.

CC -----

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CC -----

DR EMBL; AF298548; AACU5254.1; -

DR EMBL; AF310105; AAC30288.1; -

DR EMBL; AF229059; AAK00748.1; -

DR EMBL; AF229060; AAK00749.1; -

DR EMBL; AF229061; AAK00750.1; -

DR EMBL; AF229062; AAK00751.1; -

DR EMBL; AB023143; BAA76770.1; -

DR EMBL; AL117470; CAB55945.1; -

DR PIR; T17255; T17255.

DR HSP; P13489; I44Y.

DR MIM; 606636; -

DR GO; GO:0005622; C:intracellular; IC.

DR GO; GO:0016506; F:apoptosis activator activity; NAS.

DR GO; GO:0008656; F:caspace activator activity; NAS.

DR GO; GO:0019899; F:enzyme binding; IPI.

DR GO; GO:0006919; F:caspace activation; NAS.

DR GO; GO:0006917; F:induction of apoptosis; NAS.

DR InterPro; IPR001315; CARD.

DR InterPro; IPR000767; Disease_resist.

DR InterPro; IPR001611; LRR.

DR InterPro; IPR007091; LRR_RNinh.

DR InterPro; IPR007111; NACHT_Ntase.

DR InterPro; IPR004020; PAD_DAPIN_dom.

DR Pfam; PF00560; LRR; 2.

DR Pfam; PF05729; NACHT; 1.

DR Pfam; PF02758; PAD_DAPIN; 1.

DR PRINTS; PR00364; DISEASERESIST.

DR PROSITE; PS0209; CARD; 1.

DR PROSITE; PS50824; DAPIN; 1.

DR PROSITE; PS50837; NACHT; 1.

KW Apoptosis; ATP-binding; Leucine-rich repeat; Repeat;

KX Alternative splicing.

FT DOMAIN 1 92 DAPIN.

FT FT 328 637 NACHT.

FT LRR 1. 725

FT REPEAT 807 830

FT REPEAT 864 887

FT REPEAT 921 944

FT REPEAT 950 973

FT REPEAT 1199 1215

FT REPEAT 1216 1236

FT REPEAT 1374 1463

FT DOMAIN 1374 1463

FT NP_BIND 341

FT VARSPPLIC 958 987

FT VARSPPLIC 1262 1305

FT MUTAGEN 340 340

FT MUTAGEN 340 340

FT CONFLICT 155 155

FT CONFLICT 246 246

FT CONFLICT 782 782

FT CONFLICT 878 878

FT CONFLICT 995 995

FT CONFLICT 1119 1119

FT CONFLICT 1184 1184

FT CONFLICT 1241 1241

FT CONFLICT 1366 1366

FT CONFLICT 1473 AA; 165865 MW; 438F0DCE45C2562D CRC64;

SEQ SEQUENCE 1473 AA; 165865 MW; 438F0DCE45C2562D CRC64;

Query Match 57.1%; Score 216; DB 1; Length 1473;

Best Local Similarity 61.4%; Pred. No. 3.1e-17;

Matches 43; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 2 LHFIDCHRAALARTVTVNVEWLDALYGVLTDEYQAVRATNPSPKMKLFSPFPANW 61

DB 1379 LHFVDQYRQLIARTVTSVEWLDLHGVLSEQYERVLAEITRPSQMKLFPSQSWDR 1438

QY 62 TCKDLLOAL 71

DB 1439 KCKDGLYQAL 1448

RESULT 4

ASC BRARE STANDARD; PRT; 203 AA.

ID_ASC BRARE

AC Q913N6;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Apoptosis-associated speck-like protein containing a CARD (PYCARD).

GN ASC OR ASC1.

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=7995;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20373792; PubMed=10917738;

RA Tachara N. Nunez G.;

RT Genes with homology to mammalian apoptosis regulators identified in

RT Zebrafish.;

RL Cell Death Differ. 7:509-510(2000).

CC -!- FUNCTION: Promotes caspase-mediated apoptosis (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: Contains 1 DAPIN domain.

CC -!- SIMILARITY: Contains 1 CARD domain.

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RESULT 6
NOL3_MOUSE
ID NOL3_MOUSE STANDARD; PRT; 220 AA.
AC Q9D1X0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nucleolar protein 3.
GN NOL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adipose tissue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guscinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RA Functional annotation of a full-length mouse cDNA collection.;
RL Nature 409:685-690(2001).
CC -!- FUNCTION: May be involved in RNA splicing (By similarity).
CC -!- SUBUNIT: Interacts with Srp30c, NPML, CASP2, CASP8 and CED-3 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Contains 1 CARD domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL; AK021023; BAB32281.1; -.
CC MGD; MGI:1925938; NOL3.
CC InterPro; IPR001315; CARD.
CC SMART; SM00114; CARD; 1.
CC PROSITE; PS0209; CARD; 1.
CC Nucleolar protein; mRNA splicing.
CC FT DOMAIN 4 95 CARD.
CC FT DOMAIN 132 218 GLU/PRO-RICH.
CC SEQUENCE 220 AA; 24567 MW; A4DCD57C1EB320A2 CRC64;

Query Match 18.4%; Score 69.5; DB 1; Length 220;
Best Local Similarity 26.8%; Pred. No. 0.64;
Matches 22; Conservative 12; Mismatches 23; Indels 25; Gaps 3;

RESULT 7
NOL3_RAT
ID NOL3_RAT STANDARD; PRT; 221 AA.
AC Q62881;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nucleolar protein 3.
GN NOL3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain, and Pheochromocytoma;
RX MEDLINE=96221285; PubMed=8634331;
RA Geertman R., McMahon A., Sabban E.L.;
RT "Cloning and characterization of cDNAs for novel proteins with
RT glutamic acid-proline dipeptide tandem repeats.";
RL Biochim. Biophys. Acta 1306:147-152(1996).
CC -!- FUNCTION: May be involved in RNA splicing (By similarity).
CC -!- SUBUNIT: Interacts with Srp30c, NPML, CASP2, CASP8 and CED-3 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- TISSUE SPECIFICITY: Highly expressed in skeletal muscle, heart and
CC medulla.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U40627; AAB05667.1; -.
CC FIR; S70009; S70009.
CC InterPro; IPR001315; CARD.
CC SMART; SM00114; CARD; 1.
CC PROSITE; PS0209; CARD; 1.
CC Nucleolar protein; mRNA splicing.
CC FT DOMAIN 4 95 CARD.
CC FT DOMAIN 107 219 GLU/PRO-RICH.
CC SEQUENCE 221 AA; 24576 MW; A7661C9040B2CD4D CRC64;

Query Match 18.4%; Score 69.5; DB 1; Length 221;
Best Local Similarity 26.8%; Pred. No. 0.64;
Matches 22; Conservative 12; Mismatches 23; Indels 25; Gaps 3;

RESULT 8
CAR8_HUMAN
ID CAR8_HUMAN STANDARD; PRT; 431 AA.
AC Q9Y2G2; Q96P82;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caspase recruitment domain protein 8 (Apoptotic protein NDPPI) (DACAR)
DE (CARD-inhibitor of NF-kappaB activating ligand) (CARDINAL) (TUCAN).
GN CARD8 OR NDPPI OR KIAA0955.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A. (ISOFORM LONG).
RC TISSUE=Brain;
RX MEDLINE=99246063; PubMed=10231032;
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RA "Prediction of the coding sequences of unidentified human genes. XIII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro";
RL DNA Res. 6:63-70(1999).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORM LONG).
RX MEDLINE=21950691; PubMed=11821383;
RA Razmara M., Srinivasula S.M., Wang L., Poyet J.-L., Geddes B.J.,
RA Desterano P.S., Bertin J., Alnemri E.S.;
RA "CARD-8 protein, a new CARD family member that regulates caspase-1
RT activation and apoptosis";
RL J. Biol. Chem. 277:13952-13958(2002).
RN [3]
RN SEQUENCE FROM N.A. (ISOFORM LONG).
RP Zhang H.;
RA "A novel apoptotic protein, NDP1, containing CARD and BH3 domains.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A. (ISOFORM LONG).
RA Guet C., Vito P.;
RT "DACAP, a novel CARD-containing protein.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE FROM N.A. (ISOFORM LONG).
RX MEDLINE=21570185; PubMed=11551959;
RA Bouchier-Hayes L., Conroy H., Egan H., Adrain C., Creagh E.M.,
RA MacFarlane M., Martin S.J.;
RA "CARDINAL, a novel caspase recruitment domain protein, is an inhibitor
RT of multiple NF-kappa B activation pathways.";
RL J. Biol. Chem. 276:44069-44077(2001).
RN [6]
RN SEQUENCE FROM N.A. (ISOFORM SHORT).
RC TISSUE=Kidney;
RA Guo J.H., Yu L.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RN CHARACTERIZATION.
RX MEDLINE=21402909; PubMed=11408476;
RA Pathan N., Marusawa H., Krajewska M., Matsuzawa S.-I., Kim H.,
RA Okada K., Torii S., Kitada S., Krajewski S., Welsh K., Pio F.,
RA Godzik A., Reed J.C.;
RA "TUCAN, an antiapoptotic caspase-associated recruitment domain family
RT protein overexpressed in cancer.";
RL J. Biol. Chem. 276:32220-32229(2001).
RN [8]
RN CHARACTERIZATION, AND MUTAGENESIS OF LEU-366.
RX MEDLINE=22062958; PubMed=12067710;
RA Stillo R., Leonardi A., Formisano L., Di Jeso B., Vito P., Liguoro D.;
RA "TUCAN/CARDINAL and DRAL participate in a common pathway for
RT modulation of NF-kappaB activation.";
RL FEBS Lett. 521:165-169(2002).
CC -!- FUNCTION: Inhibits NF-kappa-B activation. May participate in a
CC regulatory mechanism that coordinates cellular responses
CC controlled by NF-kappa-B transcription factor. Involved in the
CC negative regulation of caspase-1.
CC -!- SUBUNIT: May form homodimers. Interacts with NEMO and DRAL. Binds
CC to caspase-1, pseudo-ICE and ICEBERG. Interacts with FENP3 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=Q9Y2G2-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=Q9Y2G2-2; Sequence=VSP_000782, VSP_000783;

CC -!- TISSUE SPECIFICITY: High expression in lung, ovary, testis and
CC placenta. Lower expression in heart, kidney and liver. Also
CC expressed in spleen, lymph node and bone marrow.
CC -!- SIMILARITY: Contains 1 CARD domain.
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CC
CC EMBL; AB023172; BAA76799.1; -
DR EMBL; AF322184; AAG50014.1; -
DR EMBL; AF331519; AAK01126.1; -
DR EMBL; AY028322; AAK08982.1; -
DR EMBL; AF405558; AAL02427.1; -
DR EMBL; AF511652; AAM46959.1; -
DR InterPro; IPR001315; CARD.
DR Pfam; PF00619; CARD; 1.
DR SMART; SM00114; CARD; 1.
DR PROSITE; PS50209; CARD; 1.
KW Apoptosis; Nuclear protein; Alternative splicing.
FT DOMAIN 340 430
FT VARSPLIC 282 286
FT VARSPLIC 287 431
FT MUTAGEN 366 366 L->R; INHIBITS HOMODIMER FORMATION.
FT CONFLICT 60 60 E -> G (IN REF. 5).
FT CONFLICT 326 326 V -> M (IN REF. 5).
FT CONFLICT 422 422 L -> P (IN REF. 5).
SQ SEQUENCE 431 AA; 48932 MW; CB54D130807732E6 CRC64;

Query Match 18.1%; Score 68.5; DB 1; Length 431;
Best Local Similarity 27.8%; Pred. No. 1.7; Mismatches 35; Indels 1; Gaps 1;
Matches 20; Conservative 16;

QY 1 GLHFDIQHRAALIAIVTNVEMLLDALY-GKVLTDQYQAVRAEPTNPMSKRLFFFTPAW 59
Db 344 GAAFKVENEHQARMGDLKGVLDLDQNEVLTEKELVQETKQSKNEALLSWVEKK 403
QY 60 NWTCKDLLLQAL 71
Db 404 GDALDVLFRSI 415

RESULT 9
ID_RIK2_MOUSE STANDARD; PRT; 539 AA.
AC P58801;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37).
GN RIKP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=21891093; PubMed=11894097;
RA Chin A.I., Dempsey P.W., Bruhn K., Miller J.F., Xu Y., Cheng G.;
RA "Involvement of receptor-interacting protein 2 in innate and adaptive
RT immune responses.";
RL Nature 416:190-194(2002).
CC -!- FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates
CC CASP-8-mediated apoptosis. Activates NF-kappaB (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Binds to CFLAR/CLARP and CASP1 via their CARD domains.

CC Binds to BIRC3/c-IAP1 and BIRC2/c-IAP2, TRAF1, TRAF2, TRAF5 and
CC TRAF6. May be a component of both the TNFRSF1A and TNFRSF5/CD40
CC receptor complex (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- PTM: Autophosphorylated (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/thr family of protein kinases.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC
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CC
CC EMBL; AF461040; AAL96436.1; -.
CC MGD; MG1:1891456; RPK2.
CC InterPro; IPR001315; CARD.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_thr_pkin_AS.
CC InterPro; IPR001245; Tyr_kinase.
CC Pfam; PF00619; CARD; 1.
CC Pfam; PF00069; pkinase; 1.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00114; CARD; 1.
CC PROSITE; PS50209; CARD; 1.
CC PROSITE; PS00111; PROTEIN KINASE DOM; 1.
CC PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
CC PROSITE; PS00108; PROTEIN KINASE ST; 1.
CC Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Apoptosis.
KW DOMAIN 18 294 PROTEIN KINASE.
FT DOMAIN 431 523 CARD.
FT NP_BIND 24 32 ATP (BY SIMILARITY).
FT BINDING 47 47 ATP (BY SIMILARITY).
FT ACT_SITE 146 146 BY SIMILARITY.
SQ SEQUENCE 539 AA; 60400 MW; 42951BF97CA15DFA CRC64;
Query Match 17.9%; Score 67.5; DB 1; Length 539;
Best Local Similarity 30.8%; Pred. No. 2.9;
Matches 16; Conservative 15; Mismatches 18; Indels 3; Gaps 2;
QV 4 FTIDHRAALIAIVTN--VEVLIDALYGX-VLTDBQYQAVRAEPTNPQKRL 52
DQ 438 WIQSKREALVQMTACLNQSLDALLSKEDYELISTKPTTSKVRQL 489
RESULT 10
BIR CHICK
ID BIR CHICK STANDARD; PRT; 611 AA.
AC Q90560; O57319;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Inhibitor of apoptosis protein (IAP) (inhibitor of T cell apoptosis
DE protein).
GN ITA OR IAPI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CC [1]
RN NCBI_TaxID=9031;
RN SEQUENCE FROM N.A.
RC TISSUE=Splice.
RX MEDLINE=97101112; PubMed=8945639;
RA Digby M.R., Kimpton W.G., York J.J., Connick T.E., Lowenthal J.W.;
RT "ITA, a vertebrate homolog of IAP that is expressed in T
RL lymphocytes.";
RN DNA Cell Biol. 15:981-988(1996).
[2]

RP SEQUENCE FROM N.A.
RC STRAIN=White Leghorn; TISSUE=Embryonic fibroblast;
RX MEDLINE=98038801; PubMed=9372964;
RA You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;
RT "ch-IAP1, a member of the inhibitor-of-apoptosis protein family, is a
RL Mol. Cell. Biol. 17:7328-7341(1997).
CC -!- FUNCTION: Apoptotic suppressor.
CC -!- SUBCELLULAR LOCATION: Predominantly nuclear. Cytoplasmic
CC according to Ref.2.
CC -!- TISSUE SPECIFICITY: Cells of the T lymphocyte lineage. Found in
CC both cortical and medullary cells of the thymus. Expressed at
CC relatively high levels also in spleen, bursa, intestine and lung
CC and at very low levels in testis, brain and skeletal muscle.
CC -!- INDUCTION: High levels are induced within 4-8 hours of T-cell
CC activation in spleen and thymus.
CC -!- DOMAIN: The ring finger is important for its antiapoptotic effect.
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 3 BIR repeats.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC
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CC
CC EMBL; U27466; AAB48118.1; -.
CC HSSP; Q13490; IQH.
CC InterPro; IPR001370; BIR.
CC InterPro; IPR001315; CARD.
CC Pfam; PF00653; BIR; 3.
CC Pfam; PF00619; CARD; 1.
CC Pfam; PF00097; zf-C3HC4; 1.
CC SMART; SM00238; BIR; 3.
CC SMART; SM00114; CARD; 1.
CC SMART; SM00184; RING; 1.
CC PROSITE; PS01282; BIR_REPEAT_1; 3.
CC PROSITE; PS0143; BIR_REPEAT_2; 3.
CC PROSITE; PS0209; CARD; 1.
CC PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
CC PROSITE; PS00089; ZF_RING_2; 1.
CC Apoptosis; Zinc-finger; Repeat; Nuclear protein.
FT REPEAT 30 97
FT REPEAT 176 242 BIR 1.
FT REPEAT 262 329 BIR 2.
FT DOMAIN 446 536 CARD.
FT ZN_FING 564 599 RING-TYPE.
FT CONFLICT 27 27 F -> L (IN REF. 2).
FT CONFLICT 150 150 R -> Q (IN REF. 2).
FT CONFLICT 169 169 Q -> H (IN REF. 2).
FT CONFLICT 183 183 S -> F (IN REF. 2).
FT CONFLICT 190 192 CLW -> FLS (IN REF. 2).
FT CONFLICT 196 196 V -> L (IN REF. 2).
FT CONFLICT 202 203 DD -> YY (IN REF. 2).
FT CONFLICT 213 214 VN -> FT (IN REF. 2).
FT CONFLICT 217 218 VK -> GO (IN REF. 2).
FT CONFLICT 350 355 WNSSCT -> EQLLS (IN REF. 2).
FT CONFLICT 359 359 K -> T (IN REF. 2).
FT CONFLICT 426 426 E -> D (IN REF. 2).
FT CONFLICT 492 492 T -> X (IN REF. 2).
FT CONFLICT 497 497 S -> L (IN REF. 2).
FT CONFLICT 524 524 F -> C (IN REF. 2).
SQ SEQUENCE 611 AA; 69009 MW; 53FC9136F34EBDDD CRC64;
Query Match 17.6%; Score 66.5; DB 1; Length 611;
Best Local Similarity 32.7%; Pred. No. 4.4;
Matches 17; Conservative 14; Mismatches 20; Indels 1; Gaps 1;

OY	2	LHFIQDRAALIRVNTNVEWLLDALY-GKVLTDQYQAVRAEPTNPSPKRL 52
DB	451	LSLIRNRNALFORLTSLPILGSLLSAKVITELEHDVIKOTTPGOAREL 502
 RESULT 11 DX52 MOUSE ID DX52 MOUSE STANDARD; PRT; 598 AA. AC Q8K3J1; Q8BV29; DT 10-OCT-2003 (Rel. 42, Created) DT 10-OCT-2003 (Rel. 42, Last sequence update) DE DEAD-box protein 52 (EC 3.6.1.-) (Putative ATP-dependent RNA helicase ROK1-like) GN DDX52 OR ROK1 OS Mus musculus [Mouse]. OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. ON NCBI_TaxId=10090; RX [1] RP SEQUENCE FROM N.A. RC TISSUE=Breast tumor; RC MEDLINE=22388257; PubMed=12477932; RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.J., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettenan M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.; RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). RN SEQUENCE OF 1-579 FROM N.A. RC STRAIN=C57BL/6J; TISSUE=Retina; RC MEDLINE=22354683; PubMed=12466851; RX Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaido I., Ootani M., Saito K., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R.P., Bult C.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Choithia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmerand S., Gustinchik S., Hirokawa N., Jackson I.J., Jarvis B.D., Kanai A., Kawaji H., Kawasaki Y., Kedziarski R.M., King B.L., Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Malais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Resole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani C., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,		

[2] SEQUENCE FROM N.A., AND MUTAGENESIS OF VAL-41 AND LYS-208.
RC TISSUE=Breast;
RX MEDLINE=99262599; PubMed=10329646;
RA Inohara N., Koseki T., del Peso L., Hu Y., Yee C., Chen S., Carrio R.,
RA Merino J., Liu D., Ni J., Nunez G.,
RT "Nod1, an Apaf-1-like activator of caspase-9 and nuclear factor-
RT kappaB";
RL J. Biol. Chem. 274:14560-14567(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP FUNCTION.
RX MEDLINE=21264704; PubMed=11058605;
RA Inohara N., Ogura Y., Chen F.F., Muto A., Nunez G.;
RT "Human Nod1 confers responsiveness to bacterial lipopolysaccharides";
RL J. Biol. Chem. 276:2551-2554(2001).
CC -!- FUNCTION: Enhances caspase-9-mediated apoptosis. Induces NF-kappa-
CC B activity via RICK (CARDIAC, RIP2) and IKK-gamma. Confers
CC responsiveness to intracellular bacterial lipopolysaccharides
CC (LPS).
CC -!- SUBUNIT: Self-associates. Binds to caspase-9 and RICK by CARD-CARD
CC interaction.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Highly expressed in adult heart, skeletal
CC muscle, pancreas, spleen and ovary. Also detected in placenta,
CC lung, liver, kidney, thymus, testis, small intestine and colon.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC -!- SIMILARITY: Contains 1 NACHT domain.
CC -!- SIMILARITY: Contains 9 leucine-rich (LRR) repeats.
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CC -----
CC EMBL; AF126484; RAD29125.1; -;
CC EMBL; AF149774; RAD43922.1; -;
CC EMBL; AF113925; RAD28350.1; -;
CC EMBL; BC040339; AAH40339.1; -;
CC Genbank; HGNC:16390; CARD4.
CC MIM; 605980; -;
CC GO; GO:0008656; F: caspase activator activity; TAS.
CC GO; GO:0006915; P: apoptosis; TAS.
CC GO; GO:0007165; P: signal transduction; TAS.
CC InterPro; IPR001315; CARD.
CC InterPro; IPR007091; LRR_RNinh.
CC InterPro; IPR007111; NACHT_NTPase.

DR Pfam; PF00619; CARD; 1.
DR Pfam; PF05729; NACHT; 1.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS0837; NACHT; 1.
KW Apoptosis; ATP-binding; Repeat; Leucine-rich repeat.
FT DOMAIN 15 105
FT CARD.
FT NP_BIND 196 531
FT ATP (POTENTIAL).
FT REPEAT 202 209
FT LRR 1.
FT REPEAT 632 656
FT LRR 2.
FT REPEAT 702 725
FT LRR 3.
FT REPEAT 727 750
FT LRR 4.
FT REPEAT 755 778
FT LRR 5.
FT REPEAT 783 806
FT LRR 6.
FT REPEAT 839 862
FT LRR 7.
FT REPEAT 867 891
FT LRR 8.
FT REPEAT 895 918
FT LRR 9.
FT REPEAT 923 946
FT MUTAGEN 41 41
FT V->Q: ABOLISHES CASPASE-9 ACTIVATION AND
FT INTERACTION WITH RICK.
FT MUTAGEN 208 208
FT K->R: REDUCES CASPASE-9 ACTIVATION.
FT CONFLICT 447 447
FT R -> H (IN REF. 3).
SQ SEQUENCE 953 AA; 107690 MW; 0A9DF5FC6487E21A CRC64;

Query Match 17.1%; Score 64.5; DB 1; Length 953;
Best Local Similarity 28.6%; Pred. No. 12;
Matches 16; Conservative 12; Mismatches 19; Indels 9; Gaps 2;

QY 2 LHFIDHRAALITARYTNVWLDALYGVLTDEQYQVRAE-----PTNPSGMRKL 52
DB 20 IQLKSNRELLVTHRNQCLVDNL-----LKNDFSAEDAELVCACPTQPKVRKI 71

RESULT 13
YGGA AERHY STANDARD; PRT; 225 AA.
AC P520J7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 24.5 kDa protein in ahyr-cdpd intergenic region.
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A1;
RX MEDLINE=97431471; PubMed=9286976;
RA Swift S., Karlyshev A.V., Fish L., Durant E.L., Winsor M.K.,
RA Chhabra S.R., Williams P., Macintyre S., Stewart G.S.B.;
RT "Quorum sensing in Aeromonas hydrophila and Aeromonas salmonicida:
RT identification of the LuxRI homologs AhyA and AhyR and their
RT cognate N-acylhomoserine lactone signal molecules";
RL J. Bacteriol. 179:5271-5281(1997).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- SIMILARITY: BELONGS TO THE LYSE/YGGA FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X89469; CAA61655.1; ALT_INIT.
CC InterPro; IPR004777; Lys_exporter.
CC InterPro; IPR001123; LYSE.
CC Pfam; PF01810; LYSE; 1.
CC TIGRFAMs; TIGR00948; 2a75; 1.
CC Hypothetical protein, Transmembrane.
CC TRANSMEM 1 21
CC POTENTIAL.
CC TRANSMEM 37 57

FT TRANSMEM 65 85 POTENTIAL.
FT TRANSMEM 116 136 POTENTIAL.
FT TRANSMEM 150 170 POTENTIAL.
SQ SEQUENCE 225 AA; 24482 MW; 172DB104473B0B09 CRC64;

Query Match 16.5%; Score 62.5; DB 1; Length 225;
Best Local Similarity 24.6%; Pred. No. 4.3;
Matches 16; Conservative 11; Mismatches 33; Indels 5; Gaps 2;

Qy 1 GLHFIDHRAAL--IARVTNVEUMLDALYGVLTDEQYQAVRAEPNPSKXKLFSTPA 58
Db 137 GSQFAELRSFAFAVAMLASLWFWYSLAFGAVLSPWLARSR---QGYSKLLILLVSPC 193

Qy 59 WNWTC 63
Db 194 WGNRC 198

RESULT 14
R1K2 HUMAN
ID -R1K2 HUMAN STANDARD; PRT; 540 AA.
AC O4353;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37)
DE (RIP-2) (CARD-containing interleukin-1 beta converting enzyme
DE associated kinase) (CARD-containing IL-1 beta ICE-kinase).
GN RIPK2 OR RICK OR RIP2 OR CARDIAK.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.
RX MEDLINE=98241596; PubMed=9575181.
RI Inohara N., del Peso L., Koseki I., Chen S., Nunez G.;
RT "RICK, a novel protein kinase containing a caspase recruitment domain,
RT interacts with CLARP and regulates CD95-mediated apoptosis.";
J. Biol. Chem. 273:12296-12300(1998).
[2]
RN SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.
RC TISSUE-Endothelial cells;
RX MEDLINE=98307936; PubMed=9642260;
RA McCarthy J.V., Ni J., Dixit V.M.;
RT "RIP2 is a novel NF-kappaB-activating and cell death-inducing
RT kinase.";
J. Biol. Chem. 273:16968-16975(1998).
[3]
RN SEQUENCE FROM N.A., AND MUTAGENESIS OF ASP-146.
RX MEDLINE=98381580; PubMed=9705938;
RA Thome M., Hofmann K., Burns K., Martinon F., Bodmer J.-L.,
RA Mattmann C., Tschoopp J.;
RT "Identification of CARDIAK, a RIP-like kinase that associates with
RT caspase-1.";
Curr. Biol. 8:885-888(1998).
[4]
RN SEQUENCE FROM N.A.
RP Oersky P., Holmes A., Broy M.;
RA Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
[5]
RN SEQUENCE FROM N.A.
RP Platzner M., Varot R.;
RA Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
[6]
RN SEQUENCE FROM N.A.
RP TISSUE=Skin;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young J.W., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates
CC CASP-8-mediated apoptosis. Activates NF-kappaB.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Binds to CFLAR/CLARP and CASP1 via their CARD domains.
CC Binds to BIRC3/c-IAP1 and BIRC2/c-IAP2, TRAF1, TRAF2, TRAF3 and
CC TRAF6. May be a component of both the TNFRSF1A and TNFRSF5/CD40
CC receptor complex.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- TISSUE SPECIFICITY: Detected in heart, brain, placenta, lung,
CC peripheral blood leukocytes, spleen, kidney, testis, prostate,
CC pancreas and lymph node.
CC -!- PTM: Autophosphorylated.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC -!- SIMILARITY: Contains 1 CARD domain.

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CC EMBL; AF027706; AAC34970.1; -;
DR EMBL; AF078530; AAC27722.1; -;
DR EMBL; AF064824; AAC25668.1; -;
DR EMBL; AC004003; AAC24561.1; -;
DR EMBL; AF117829; RAD04634.1; -;
DR EMBL; BC004553; AAH04553.1; -;
DR Genew; HGNC:10020; RIPK2.
DR MIM; 603455; -;
DR GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
DR GO; GO:0004871; F:signal transducer activity; TAS.
DR GO; GO:0006915; P:apoptosis; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR GO; GO:0007165; F:signal transduction; TAS.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR InterPro; IPR01245; Tyr_pkinase.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00669; Pkinase; 1.
DR PRINTS; PR0109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00114; CARD; 1.
DR PROSITE; PS00209; CARD; 1.
DR PROSITE; PS00117; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Apoptosis.
FT DOMAIN 18 294 PROTEIN KINASE.
FT DOMAIN 432 524 CARD.
FT NP_BIND 24 32 ATP (BY SIMILARITY).
FT BINDING 47 47 ATP.
FT ACT_SITE 146 146
FT MUTAGEN 47 47 K->A: ABOLISHES KINASE ACTIVITY.

Job time : 7.84337 secs

FT MUTAGEN 47 47 K->M: REDUCES FAS-MEDIATED APOPTOSIS.
FT MUTAGEN 146 146 D->N: ABOLISHES KINASE ACTIVITY.
SQ SEQUENCE 540 AA: 61194 MW; 575A692239505792 CRC64;

Query Match 16.5%; Score 62.5; DB 1; Length 540;
Best Local Similarity 30.4%; Pred. No. 11;
Matches 17; Conservative 13; Mismatches 23; Indels 3; Gaps 2;

QY 4 FIDQHRALAIARVTN--VEWLLDALYK-VLTDEQYQAVRAEPTNPSKMKRLFSFT 56
Db 439 WIQSKREDIVNQMTBACLNSLDALLSRDLIMKEDYELVSTKPTRTSKVQQLDIT 494

RESULT 15

ID DX52 RAT STANDARD; PRT; 598 AA.
AC Q99PT0;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE DEAD-box protein 52 (EC 3.6.1.1-) (Putative ATP-dependent RNA helicase ROK1-like) (rROK1L).
GN DDX52 OR ROK1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Li W., Suzuki T.;
RT "Identification of a novel ROK1-like protein in rat brain."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
CC -!- SIMILARITY: Belongs to the DEAD box helicase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/) or send an email to license@isb-sib.ch).
CC -----

DR EMBL; AB055628; BAB32441.1; -.
DR HSP; Q58083; 1HV8.
DR InterPro; IPR001410; DEAD.
DR Pfam; PF001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELICC; 1.
DR PROSITE; PS00039; DEAD_ATP_HELICASE; FALSE NEG.
KW Hydrolase; Helicase; Nuclear protein; RNA-binding; ATP-binding.
FT NP_BIND 210 217 ATP (BY SIMILARITY).
FT SITE 319 322 DEAD BOX.
FT DOMAIN 86 92 POLY-LYS.
SQ SEQUENCE 598 AA: 67239 MW; B9E819EA6B144425 CRC64;

Query Match 16.4%; Score 62; DB 1; Length 598;
Best Local Similarity 25.0%; Pred. No. 14;
Matches 26; Conservative 15; Mismatches 19; Indels 44; Gaps 6;

QY 2 LHFIDQHRALAIAR-----VTNVEWLL----DA 25
Db 266 LHWI--HKAATAAKFKPKSKKEDILVTNRLIYLKQPPGIDLTSEVWLVVDSK 323
QY 26 LY--GKVLTDQYQAVRAEPTNPSKMKRLFSFTPAWN---WTCK 64
Db 324 LFEDGKTGFRDQLASIFLACTSPKVRRAWFSAITFAYDVEQW-CK 366

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2004, 08:49:47 ; Search time 28.2289 Seconds
(without alignments)
793.576 Million cell updates/sec

Title: us-09-996-617-8_COPY_111_181
Perfect score: 378
Sequence: 1 GHFIDQRAALIARVNVVE.....LSFTFPAWNTCKDLLLQAL 71

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	303	80.2	195	6 Q8HXK9	Q8HXK9 bos taurus
2	269	71.2	193	11 Q8CHK8	Q8CHK8 rattus norv
3	73.5	19.4	220	11 Q8C550	Q8C550 mus musculus
4	69.5	18.4	220	11 Q8R283	Q8R283 mus musculus
5	68	18.0	449	16 Q88WC4	Q88WC4 lactobacill
6	68	18.0	545	16 Q9CBL2	Q9CBL2 mycobacteri
7	67	17.7	257	4 Q9H695	Q9H695 homo sapien
8	67	17.7	912	15 Q90278	Q90278 chimpanzee
9	67	17.7	1175	16 Q8XNW6	Q8XNW6 cleistridium
10	66.5	17.6	1170	16 Q882B7	Q882B7 pseudomonas
11	66	17.5	249	4 Q8N528	Q8N528 homo sapien
12	65.5	17.3	149	16 Q8FTY0	Q8FTY0 corynebacte
13	65.5	17.3	616	13 Q804E2	Q804E2 ictalurus p
14	65.5	17.3	628	13 Q8UWD2	Q8UWD2 brachydanic
15	65.5	17.3	647	13 Q7T0K2	Q7T0K2 brachydanic
16	65	17.2	1134	16 Q8PEL2	Q8PEL2 xanthomonas

17	64.5	17.1	597	10 Q9ZSB8	Q9ZSB8 arabidopsis
18	64.5	17.1	605	10 Q9T0C0	Q9T0C0 arabidopsis
19	64	16.9	304	16 Q9PU91	Q9PU91 campylobact
20	63.5	16.8	285	16 Q8PEI0	Q8PEI0 xanthomonas
21	63.5	16.8	456	13 Q9W7D6	Q9W7D6 oryzias lat
22	63	16.7	565	2 Q9KJ20	Q9KJ20 actinopolys
23	63	16.7	955	16 Q8A654	Q8A654 bacteroides
24	63	16.7	1134	16 Q8P378	Q8P378 xanthomonas
25	62.5	16.5	602	11 Q9SEB9	Q9SEB9 rattus norv
26	62.5	16.5	610	13 Q57319	Q57319 gallus gall
27	62	16.4	779	16 Q8YN00	Q8YN00 anabaena sp
28	61.5	16.3	128	2 Q8GHU3	Q8GHU3 pseudomonas
29	61.5	16.3	280	16 Q8P342	Q8P342 xanthomonas
30	61.5	16.3	306	5 Q19619	Q19619 caenorhabdi
31	61.5	16.3	650	2 Q52870	Q52870 rhizobium 1
32	61.5	16.3	1193	5 Q19617	Q19617 caenorhabdi
33	61.5	16.3	3729	2 Q33956	Q33956 streptomyce
34	61	16.1	277	16 Q9I6Q4	Q9I6Q4 pseudomonas
35	61	16.1	321	11 Q8BUR0	Q8BUR0 mus musculu
36	61	16.1	326	16 Q9KZK7	Q9KZK7 streptomyce
37	61	16.1	338	16 Q8ZDY2	Q8ZDY2 versinia pe
38	61	16.1	342	11 Q8D8L8	Q8D8L8 mus musculu
39	61	16.1	345	12 Q84439	Q84439 paramecium
40	61	16.1	353	16 Q82NU4	Q82NU4 streptomyce
41	61	16.1	359	11 Q9D3N8	Q9D3N8 mus musculu
42	61	16.1	666	2 Q9RHG7	Q9RHG7 bacillus ce
43	61	16.1	983	2 Q9KDX6	Q9KDX6 bacillus me
44	61	16.1	983	2 Q93R39	Q93R39 bacillus ce
45	60.5	16.0	290	11 Q921C9	Q921C9 cricetus

ALIGNMENTS

RESULT 1

Q8HXK9 ID Q8HXK9 PRELIMINARY; PRT; 195 AA.
AC Q8HXK9;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Apoptosis-associated speck-like protein containing a CARD.
GN BASC.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Masumoto J., Zhou W., Chen F.F., Su F., Kuwada J.Y., Hidaka E.,
RA Katsuyama T., Sagara J., Taniguchi S., Nago-Hazelett P.,
RA Postlethwait J.H., Nunez G., Inohara N.,
RT "Casp-1: A Zebrafish caspase activated by ASC oligomerization required
RT for pharyngeal Arch development.",
RL J. Biol. Chem. 274:33835-33838(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Masumoto J., Taniguchi S., Ayukawa K., Sarvotham H., Kishino T.,
RA Masumoto J., Taniguchi S., Ayukawa K., Higurashi T., Sagara J.,
RA Naito N., Hidaka E., Katsuyama T., Higurashi T., Sagara J.,
RT "ASC, a novel 22-kDa protein, aggregates during apoptosis of human
RT promyelocytic leukemia HL-60 cells.",
RL J. Biol. Chem. 274:33835-33838(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Masumoto J., Taniguchi S., Nakayama K., Ayukawa K., Sagara J.,
RT "Murine ortholog of ASC, a CARD-containing protein, self-associates,
RT and exhibits restricted distribution in developing mouse embryos.",
RL Exp. Cell Res. 262:128-133(2001).
DR EMBL; ARS00006; BAC43753.1;
DR GO; GO:0005622; C:intracellular; IEA.


```
Qy 57 -----PAWNW 61
Db 72 ACQELLRCQQTVMRPPDPAW 93

RESULT 5
Q88WC4 PRELIMINARY; PRT; 449 AA.
AC Q88WC4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Aminotransferase (EC 2.6.1.-).
GN LP_1721.
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIMB 8826 / WCFS1;
RX MEDLINE=22480296; PubMed=12566566;
RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
RA De Vos W.M., Siezen R.J.;
RT "Complete genome sequence of Lactobacillus plantarum WCFS1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
DR EMBL; AL935257; CAD64145.1; -.
DR GO; GO:0008483; F:transaminase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR005814; Aminotrans_3.
DR Pfam; PF00202; aminotran_3; 1.
DR Aminotransferase; Transferase; Complete proteome.
KW AMINOTRANSFERASE; TRANSFERASE;
SQ SEQUENCE 449 AA; 49491 MW; E2C04FEF25F69E0C CRC64;

Query Match 18.0%; Score 68; DB 16; Length 449;
Best Local Similarity 27.2%; Pred. No. 7.7;
Matches 22; Conservative 13; Mismatches 22; Indels 24; Gaps 4;

Qy 3 HFIDQ-----HRAALIARTVNEWLLDALYGVLTDSQYVAQVRAEPTN 45
Db 6 HRLDQQLIEREDHYWATARYNYDLVIDHAGALLTVDGNYIDLLASASAINVGHTH 65

Qy 46 PSXMR-----KLPSTPAW 59
Db 66 PRVVAIQEQAAKLIHTPAY 86

RESULT 6
Q9CBL2 PRELIMINARY; PRT; 545 AA.
AC Q9CBL2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ABC transporter ATP-binding protein, possibly in EF-3 subfamily.
GN M1816.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eigmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
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RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
DR EMBL; AL583923; CAC30769.1; -.
DR PIR; A87136; A87136.
DR Leproma; M1816; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA-ATPase.
DR InterPro; IPR003439; ABC transporter.
DR Pfam; PF00005; ABC tran; 2.
DR ProDom; PD000006; ABC transporter; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00211; ABC TRANSPORTER_1; 2.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 545 AA; 58986 MW; 75AAA463EB91FBCD CRC64;

Query Match 18.0%; Score 68; DB 16; Length 545;
Best Local Similarity 36.4%; Pred. No. 9.7;
Matches 20; Conservative 3; Mismatches 16; Indels 16; Gaps 2;

Qy 8 HRAALIARTVNEWLLDALYGV-----LTDEYQAVRAEPTNPSK 48
Db 226 HNELIAAVARVWFLDAVLGKVDYVNGWYKYLDSRATDEQRR--RRERVNAER 278

RESULT 7
Q9H695 PRELIMINARY; PRT; 257 AA.
AC Q9H695;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein FLJ22474.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Ota T., Suzuki Y., Oabayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RL "NEDO human cDNA sequencing project.";
RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK026127; BAB15368.1; -.
DR Genew; HGNC:20310; GRTPL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR000195; RabGAP_TBC.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00566; TBC; 1.
DR SMART; SM00164; TBC; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
DR PROSITE; PS00886; TBC_RABGAP; 1.
KW Hypothetical protein.
SQ SEQUENCE 257 AA; 28960 MW; 5B0A7B5779DF2B94 CRC64;

Query Match 17.7%; Score 67; DB 4; Length 257;
Best Local Similarity 33.9%; Pred. No. 5.2;
Matches 19; Conservative 10; Mismatches 19; Indels 8; Gaps 2;

Qy 1 GLHFIDQHRAALIARTVNE-----WLLDALYGVLTDSQYVAQVRAEPTNPSKRL 52
Db 69 GNMFI----AGYLVLTITNEEESFWLLDALVGRILPDYSPAMGLKTDQVIGEL 120
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RESULT 8
O90278      PRELIMINARY;      PRT;      912 AA.
ID AC O90278;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope protein.
GN ENV.
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11723;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SIVhoest;
RX MEDLINE=9908990; PubMed=9882304;
RA Hirsch V.M., Campbell B.J., Bailes E., Goeken R., Brown C.,
RA Elkins W.R., Axthelm M., Murphey-Corb M., Sharp P.M.;
RT "Characterization of a novel simian immunodeficiency virus (SIV) from
RT L'Hoest monkeys (Cercopithecus l'hoesti): implications for the origins
RT of SIVmd and other primate lentiviruses.";
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SIVhoest;
RA Hirsch V.M.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF075269; RAD12149.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR00777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 912 AA; 104904 MW; 70F8E016922DAAC CRC64;

Query Match      17.7%; Score 67; DB 15; Length 912;
Best Local Similarity 29.0%; Pred. No. 24;
Matches 18; Conservative 7; Mismatches 19; Indels 18; Gaps 2;

QY 17 TNVEWLLD-----ALYGVLTDEQVAVRAEPTNSMKRKLFSFPPAW 59
D5 642 TNVETYNITPNWTKDTWREWSKVAYIDKNITSLQEAFTLELNQKFKLQEFN-FW 700
QY 60 NW 61
D5 701 SW 702

RESULT 9
Q8XNW6      PRELIMINARY;      PRT;      1175 AA.
ID AC Q8XNW6;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Probable exonuclease.
GN SBCC OR CPE0216.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / Type A; PubMed=11792842;
RX MEDLINE=21664373; PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Oshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic

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RT flesh-eater."
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; AF003185; BAB79922.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; IEA.
DR GO; GO:0004527; F:exonuclease activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC_transporter.
KW Exonuclease; Complete proteome.
SQ SEQUENCE 1175 AA; 136878 MW; 7C6D2366525019C1 CRC64;

Query Match      17.7%; Score 67; DB 16; Length 1175;
Best Local Similarity 36.2%; Pred. No. 33;
Matches 17; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

QY 5 IQCHRAALIAIVTVVWLLDALYGVLTDEQVAVRAEPTNSMKRKL 51
D5 924 IBEYDNNLIKANIELLIKNGKSLTEETRVLQEKNTKELK 970

RESULT 10
Q882B7      PRELIMINARY;      PRT;      1170 AA.
ID AC Q882B7;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Sensor histidine kinase/response regulator.
GN PSP02712.
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RA Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
RA Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,
RA Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
RA Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,
RA White O., Fraser C., Collier A.;
RT "Complete sequence of Pseudomonas syringae."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB018665; AAC56213.1; -.
DR TIGR; PSP02712; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0016304; F:kinase activity; IEA.
DR GO; GO:0008289; F:lipid binding; IEA.
DR GO; GO:0000156; F:two-component response regulator activity; IEA.
DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000160; P:two-component signal transduction system (p. .; IEA.
DR InterPro; IPR003594; ATPbind ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR007891; CHASE3.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR003661; His_kinase.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF05227; CHASE3; 1.
DR Pfam; PF01590; GAF; 1.
DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF00512; HSKA; 1.
DR Pfam; PF00072; response_reg; 3.
DR PRINTS; PR00344; BCTELSENSOR.
DR PROSITE; PS00214; FADP; 1.

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RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Kawabayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Uda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens YS-314.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RD ENBL: AP005214; BAC17053.1; -.
RW Hypothetical protein; Complete proteome.
SQ SEQUENCE 149 AA; 16334 MW; DL1861ADB491A4F5 CRC64;

Query Match 17.3%; Score 65.5; DB 16; Length 149;
Best Local Similarity 32.7%; Pred. No. 4.1;
Matches 17; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

Qy 7 CHRAALIAIYTVNVE-WLLDALYCKVLTEYOYCAVRAEPTPSKMRKLPST 56
Db 99 QHKSASTASTELSHLWISASTQILLAD-TYSVIPADDSVENLMRTFGWT 149

RESULT 13
ID Q804E2 PRELIMINARY; PRT; 616 AA.
AC Q804E2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Inhibitor of apoptosis protein-1.
GN CIAP-1.
OS Itcalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
CX NCBI_TaxID=7998;
[1]
RP SEQUENCE FROM N.A.
RA Praven K. Leary J.H. III, Evans D.L., Jaso-Friedmann L.;
RL "Cloning of anti-apoptotic genes in non-specific cytotoxic cells.";
RD ENBL: AY184377; AAC24632.1; -.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO: GO:0006916; P:anti-apoptosis; IEA.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00194; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
SQ SEQUENCE 616 AA; 69546 MW; DL1389D915C6BB256 CRC64;

Query Match 17.3%; Score 65.5; DB 13; Length 616;
Best Local Similarity 34.1%; Pred. No. 23;
Matches 14; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

Qy 1 GLHFIDGHRALIAIYTVNVEWLLDALYCK-VLTDEQYQAVR 40
Db 455 GFTFLKHHALTORLKSQVSLMDHLLLENVISQKEYDTR 495

RESULT 14
ID Q8UND2 PRELIMINARY; PRT; 628 AA.
AC Q8UND2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

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